

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_nzp model

Run on: June 15, 2005, 02:16:48 ; Search time 183 Seconds
(without alignments)
10947.644 Million cell updates/sec

Title: US-10-775-627A-3
Perfect score: 4611
Sequence: 1 ctcgagattacccttaccag.....ctcttctcttctctctc 2590

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonum62 -TRANS=human40.cdi
-LIST=5 -DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=20
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-NO_MMAP -LARGEOBURY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_GeneSeq.16Dec04:*
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2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2809	60.9	545	5	ABB08276 Murine mu
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4	1922.5	41.7	452	7	ADB64249 Human MUR
5	1763	38.2	412	7	ADCC1770 Human MUR
6	1735.5	37.6	414	4	AAU15868 Human nov
7	1735.5	37.6	414	6	ABU54937 Human nov
8	1166	25.3	358	4	AAE63832 Human nov
9	1166	25.3	358	7	AAE63832 Human nov
10	1166	25.3	358	7	ADCC1154 Human nov

11	1162	25.2	366	5	ABB08275	Abb08275 Murine mu
12	1140.5	24.7	366	3	AAE21048	Abb21048 Human nuc
13	1139.5	24.7	366	4	AAU25438	AAU25438 Human mtd
14	1131	24.5	400	5	ABB81144	Abb81144 Human MUR
15	1121	24.3	351	5	ABB81134	Abb81134 Rat MURF1
16	1095.5	23.8	370	4	AAU00918	AAU00918 Human bon
17	1088.5	23.6	353	4	ABE50234	Abb50234 Human tra
18	1088.5	23.6	353	5	ABG93804	Abg93804 Human bon
19	1088.5	23.6	353	6	ADA55293	Ada55293 Human pro
20	1088.5	23.6	353	7	ADE61549	Ad661549 Human pro
21	1088.5	23.6	353	7	ADE61546	Ad661546 Human pro
22	1086	23.6	289	5	ABB81145	Abb81145 Human MUR
23	1086	23.6	340	5	ABB81135	Abb81135 Human MUR
24	1082.5	23.5	366	6	AAU15855	AAU15855 Human nov
25	1082.5	23.5	366	6	ABU54924	Abu54924 Human nov
26	1082	23.5	343	5	ABB08277	Abb08277 Murine mu
27	1022	22.2	326	5	ABB83475	AAU009475 Human cyt
28	949	20.6	302	4	AAU00998	AAU00998 Human bon
29	918	19.9	254	4	AAU61322	AAU61322 Human tra
30	871.5	18.9	602	8	ADP22642	Sea-squir
31	817	17.7	181	7	ADCC3320	Human nov
32	788	17.1	201	5	ABB81142	Abb81142 Rat MURF1
33	786	17.0	184	6	AAU16327	AAU16327 Human nov
34	786	17.0	184	6	ABU55396	Abu55396 Human nov
35	634.5	13.8	143	3	AAU841076	AAU841076 Human ORF
36	634.5	13.8	143	5	ABP34078	Abp34078 Human int
37	485	10.5	122	3	AAU841760	AAU841760 Human ORF
38	459	10.0	716	7	ADD01211	ADD01211 Human nuc
39	448	9.7	719	6	ADA14349	Ada14349 Mouse spe
40	436	9.5	667	8	ADQ21458	Adq21458 Human sof
41	432.5	9.4	552	7	ADJ70562	Adj70562 Human hea
42	431	9.3	685	4	AAU79101	AAU79101 Human pro
43	431	9.3	685	4	ABG18060	Abg18060 Novel hum
44	431	9.3	744	4	ABG18061	Abg18061 Novel hum
45	420	9.1	524	8	ADR09855	Adr09855 Human pro

ALIGNMENTS

RESULT 1	ABE08276	standard; protein; 545 AA.
ID	ABB08276	
XX	ABB08276	
AC	ABB08276	
XX	15-JUL-2002	(first entry)
XX	15-JUL-2002	
DE	Murine muscle ring finger protein 2 (MURF-2).	
XX		
KW	Muscle ring finger; MURF-2; mouse; cardiant; microtubule;	
KW	intermediate filament; striated muscle; cardiac hypertrophy;	
KW	heart disease.	
XX		
OS	Mus musculus.	
XX		
PN	W0200206318-A2.	
XX		
PD	24-JAN-2002.	
XX		
PF	18-JUL-2001; 2001WO-US022896.	
XX		
PR	18-JUL-2000; 2000US-0219020P.	
XX		
PA	(TEXA) UNIV TEXAS SYSTEM.	
XX		
PI	Olson EN, Spencer JA;	
XX		
DR	WPI: 2002-241506/29.	
XX		
DR	N-PSDB; ABA99062.	
XX		
PT	Novel muscle ring finger protein useful for drug screening, and for	
XX	diagnosing and treating diseases, particularly cardiomyopathies.	

PS Claim 42; Fig 10; 134pp; English.

XX The sequence represents murine muscle ring finger protein 2 (MURF-2). The
CC invention relates to a purified muscle ring finger (MURF) protein,
CC selected from MURF-1, MURF-2 and MURF-3. The MURF proteins of the
CC invention are involved in microtubule and intermediate filament
CC stabilisation of striated muscle cells and have cardiant activity. The
CC MURF proteins are useful for screening a candidate substance for MURF
CC protein-binding activity, in a cell, cell-free system or in vivo, and its
CC effect on interaction of MURF with microtubules, homodimerisation of
CC MURF, MURF-1, MURF-2 or MURF-3 stabilisation of microtubules, interaction
CC of MURF with intermediate filaments, e.g. desmin, vimentin and
CC cyokeratin, and heterodimerisation of MURF. The screened compounds are
CC useful for treating and preventing cardiac hypertrophy and heart
CC diseases. MURF proteins are useful as antigens to immunise animals for
CC the production of antibodies

XX Sequence 545 AA;

Alignment Scores:

Pred. No.:	4.34e-227	Length:	545
Score:	2809.00	Matches:	545
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	60.92%	Indels:	0
DB:	5	Gaps:	0

US-10-775-627A-3 (1-2590) x ABB08276 (1-545)

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QY 140 GAAAGCAACTGATCTGTCCCATCTGCTAGAGATGTCACGAAAGCTGTGTATTC 199
Db 21 GlnLysGlnLeuIleCysProIleCysLeuGlnMetPheTrpValIleLeu 40
QY 200 CTTTCGACGACAACTGTGACGAAATGTGCAGTGAATCTTCAGAGCTCTAACCCG 259
Db 41 ProCysGlnHisAsnLeuCysArgLysCysAlaSerAspIlePheGlnAlaSerAsnPro 60
QY 260 TACTTATCCCAAGAGAGAGGACCAACCGTGCATAGAGGGCCGCTTCCTGTCCTCC 319
Db 61 TyrLeuProThrArgGlyGlyThrValAlaSerGlyArgPheArgCysPheSer 80
QY 320 TGACAGCATGAGTGTGTAGACAGACATGAGGAGCTATGAGCTGCAGAGAACCTGCTC 379
Db 81 CysArgHisGlnValValLeuAspArgHisGlyValIleGlyLeuGlnArgAsnLeu 100
QY 380 GTGAAAAACATTATGATATCTACAGAGAGAAATCCACAGAGCCAGAAAAAATTGAC 439
Db 101 ValGlnAsnIleIleAspIleTyrLysGlnGlnSerThrArgProGlnLysLeuAsp 120
QY 440 CAGGCCATGTGTGAAGACATGAAGAGAGAGACATCAATCTATGTCTGAATCTGAA 499
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QY 500 GTGCCACACTGCTCTGTGCAAGGTTTGTGGCGCCATAAGAGACTGCAGAGTGGCTCC 559
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QY 620 GGAAGCAACGATTAGAGTCAAGGAGTGTGATCAAGCCAGCTGAGAGACACTGTAAACTATT 679
Db 181 GlySerAsnAspArgValGlnGlyValIleSerGlnLeuGlnAspThrCysLysThrIle 200
QY 680 GAGAGTCTGACAGAAACAGAAACAGGACCTGTGTGAGAAATTGATCACCTATACGCG 739
Db 201 GlnGlnCysCysArgLysGlnLysGlnAspLeuCysGlnLysPheAspHisLeuTyrIle 220
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QY 1100 GAAGAAAGAGAGAGAGAGATGCACTAGAACTAGAAAGAGAGAGAGAGAGAGAGAG 1159
Db 341 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 360
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Db 361 SerSerLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 380
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Db 381 LeuGlnValAlaProGlnProLeuProAlaSerSerProGlnProPheSerSerMetPro 400
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Db 401 ProAlaIleAspValLeuValIleThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 420
QY 1340 AACAAGCTGAAACTTACAGCCCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1399
Db 421 ThrGlnSerGlnThrSerGlnProSerAlaIleGlnThrAlaAspProLeuPheTyrPro 440
QY 1400 AGTTGATATAAGGCGCAAGCCGAGAAACAGAGCTCAACCACTTCATCAGTGGAGT 1459
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QY 1460 GAAGGTCTGGGTCAAATAGGAGCTCTGGGCAATTGAGGATTCAGATGTCAGTCCGAGAA 1519
Db 461 GlnGlnLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 480
QY 1520 GTGCAGAGAGCCGAGAACCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1579
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QY 1580 GCAGCTACTCTCAGATTGATTTGAGGCGCTTCTCCAGAGGAGACAGTGCAGCTTG 1639
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QY 1640 GGGAGTGGGGGTGGGATCTGAGCCAGCTGCACAGTCTTCTCTCTCTGCTGTTG 1699
Db 521 GlySerGlyGlyValIleLeuSerGlnLeuAlaThrSerSerProSerProGlnLysLeu 540
QY 1700 AATTCCCTAAATGAA 1714
Db 541 AsnSerLeuAsnGln 545
RESULT 2
ADB64489
ID ADB64489 standard; protein; 548 AA.
XX
AC ADB64489;
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XX 04-DEC-2003 (first entry)
DT Human protein encoded by clone HEART20019310.
DE
XX Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
XX cell regeneration; membrane protein; signal transduction-related protein;
XX transcription-related protein; osteoporosis; neurological disease;
XX cancer; tumour.
OS Homo sapiens.
XX EP1308459-A2.
XX
XX 07-MAY-2003.
XX
XX 28-MAR-2002; 2002EP-00007401.
XX
XX 05-NOV-2001; 2001JP-00379298.
PR 25-JAN-2002; 2002US-00350978.
XX
XX (HELI-) HELIX RES INST.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto Y, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;
XX
XX WPI; 2003-450961/43.
DR N-PSDB; ADB62519.
XX
XX New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX
XX Claim 1; Page; 222pp; English.
XX
XX The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesising the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.
XX
XX Sequence 548 AA;
SQ

Alignment Scores:
Pred. No.: 3,02e-189 Length: 548
Score: 2359.50 Matches: 465
Percent Similarity: 90.56% Conservativeness: 34
Best Local Similarity: 84.39% Mismatches: 44
Query Match: 51.17% Indels: 9
DB: 7 Gaps: 3

US-10-775-627A-3 (1-2590) X ADB64489 (1-548)

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DB 1 MetSerAlaSerLeuLeuValGlySerPheSerLeuGluGlnInhrMetAspAsnLeu 20
QY 140 GAAAGCAACTGATCTGTCTCCATCTGCTAGAGATGTTCAAGAGCCTGTGATCTTC 199
DB 21 GluValGlnLeuLeuLeuCysProIleCysLeuGlnMetPheThrIysProValIleLeu 40
QY 200 CTTTGCCAGACCAACTGTGACAGAAATGTCAGTACATCTTCCAGGCTCTTAACCG 259
DB 41 ProCysGlnHisAsnLeuCysArgLysCysAlaSerAspIlePheGlnAlaSerAspPro 60
QY 260 TACTTACCCAGAGAGAGGACACACCGGGCATCAGGGGGCGCTTCCGCTGCCCTCC 319
DB 61 TyrLeuProThrArgGlyGlyGlnThrMetAlaSerGlyValArgPheArgCysProSer 80
QY 320 TGCAGACATGAGGCTGTGTAGACAGACATGGGGCTATGACTGACAGAGAACTGCTC 379
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QY 380 GTGAAAACATTTATGATATCTACAGACAGAAATCCACAGGCCAGAAAAAATTGAC 439
DB 101 ValGluAsnIleIleAspIleTyrLysGlnGlnSerThrArgProGluLysSerAsp 120
QY 440 CAGCCCATGCTGTAAGAGCATGAAAGGAAACGATCAACATCTATTGCTGACCTGGAA 499
DB 121 GlnProMetCysGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 140
QY 500 GTGCCCACTGTCTCTTGTGACAGGTTTGTGGCCCATGAAAGAGCTGCCAGTGCTCCC 559
DB 141 ValProThrCysSerLeuGlyValPheGlyValHisValAspArgCysGlnValAlaPro 160
QY 560 CTGACTCATGTGTTCAGAGCAGAAAGTCAAGACTCACTGATGATGCTGTACTTGTG 619
DB 161 LeuThrHisValPheGlnArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
QY 620 GAAAGCAACATGAGTGCAGGGGTGATGAGCAGCTGGAGAGACCTGTAAACATAT 679
DB 181 GlySerHisAspArgValGlnGlyValIleSerGlnLeuGlnAspThrCysLysThrIle 200
QY 680 GAGAGTGTCTGCAAGAAAGCAGAAAGCAGACTGTGTGAGAAATTTGATCACTTACGAC 739
DB 201 GluGlnCysSerArgLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 220
QY 740 ATCTTGAGAGAGAGAAAGTGAATGACCAACCATCTGTAACACAGAGAGAAA 799
DB 221 IleLeuGlnGlnIuArgLysAsnGlnMetThrGlnValIleThrArgThrGlnGlnGln 240
QY 800 CTGGAACATGTCGGAACCTCTTATCAGAGATTCGATCAGCTGGAGAGACGTATCCCAAG 859
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QY 860 TTGTGAGAGTCAAGAAATCCAGTTCATGATGAGCCGCAAAATGACAGATTTCTGCAAGAT 919
DB 261 LeuValGlnSerIleGlnGlnPheMetAspGlnProGlnMetAlaValPheLeuGlnAsn 280
QY 920 GCCAAGACCTGTGCAAAAAGATCTGGAAGCATCAAAAGCGCTTTCAGATGAGAAACTA 979
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QY 1040 ATCCGTGAATTAATGACTTTTCTAGA-----GAAGAGGAAGAGGAAGATGAGAGAA 1093
DB 321 IleArgGlnIleAspPheTyrArgGlnAspGlnAspGlnGlnGlnGlnGlnGlnGln 340
QY 1094 ATGAGTAAGAGAGAGAGAGAG-----GATGCACTAGAAAGTGAAGAGGACGAGA 1144
DB 341 GlyGlnLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 360

[illegible]

PI Elliott VS, Burford N, Ding L, Yue H, Becha S, Emerling BM,
 PI Richardson TW, Lee SY, Bandman O, Lai PG, Lee S, Gietzen KU,
 PI Walla NK, Griffin JA, Lee EA, Swarnakar A, Ring HZ, Jones KA,
 DR MPI: 2003-092894/08.
 DR N-PSDB; AMD49597.
 XX
 PT New human cytoskeleton-associated proteins, useful for preparing a
 PT composition for diagnosing or treating a disease or condition associated
 PT with decreased expression or overexpression of functional CSAP e.g.,
 PT cancer.
 PS
 PS Claim 1, Page 165-166; 233pp; English.
 XX
 CC The invention relates to new human cytoskeleton-associated protein (CSAP)
 CC and its polynucleotide. The polypeptide is useful for preparing a
 CC composition for diagnosing or treating a disease or condition associated
 CC with decreased expression or overexpression of functional CSAP e.g.,
 CC atherosclerosis or cancer. The present sequence is human CSAP-8 protein.
 CC The invention is useful in gene therapy
 CC
 SQ Sequence 452 AA;
 SQ
 Alignment Scores:
 Pred. No.: 1.7e-152 Length: 452
 Score: 1922.50 Matches: 332
 Percent Similarity: 75.14% Conservative: 22
 Best Local Similarity: 71.14% Mismatches: 33
 Query Match: 41.69% Indels: 105
 DB: Gaps: 4
 US-10-775-627A-3 (1-2590) x AAE32110 (1-452)
 QY 80 ATGACACACTTCCTGGAATTATACAAAGCTTTCTCCAAAGACACAGACCAATGATACTTG 139
 Db 1 MetSerAlaSerLeuAsnTrpLysSerPheSerLysGluGlnGlnThrMetCysAsnLeu 20
 QY 140 GAAAAGCACTGATGTGTGCCATCTGCGCTTGAAGATGTTTACGAAAGCCTGTGCTATTCTC 199
 Db 21 GluLysGlnLeuIleCysProIleCysLeuGlnMetPheThrIleProValIleLeu 40
 QY 200 CTTTGCCACACAACTGTGACGAAATGTGCCAGTGAATCTTCCAGGCTTTAACCCG 259
 Db 41 ProCysGlnHisAsnLeuCysArgLysCysAlaSerAspIlePheGlnAlaSerAsnPro 60
 QY 260 TACTTACCCACAAAGAGAGACCAACCGGATGATAGAGGGGGCGCTTCCGCTGCTCCCTCC 319
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 QY 320 TCCAGACATGAGTGGTGTGAACAGACATCGGGGTCTATGACTGCAGAGAACTGCTC 379
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 QY 380 GTGGAACAACTATTGATGATCTTACAAAGACGAAATCCACAGGCCAGAAAAAATTGGAC 439
 Db 101 ValGlnAsnIleIleAspIleTyrLysGlnGlnSerThrArgProGlnLysSerAsp 120
 QY 440 CAGCCCATGTGTGAAGAGCATGAAGAGAACCCATCAACATGATATTGTGTGAATGTGAA 499
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 QY 500 GTGCCCACTGTCTCTTGTGCAAGGTTTTTGAGCGCCAAAGAAGCTGCCAGTGGCTCC 559
 Db 141 ValProThrCysSerLeuCysLysValPheGlyAlaHisLysAspArgGlyIleAlaIleVal 160
 QY 560 CTGATCTATGTTTCCAGAGCAGAGAGTACAGAGCTCAGTGAAGGTATTCTGTACTGTG 619
 Db 161 LeuThrHisValPheGlnArgGlnLysSerGlnLeuSerAspGlyIleAlaIleVal 180
 QY 620 GGAAGCAACATAGATGCCAGGGTGTGATCAGCAGACTGAGAGACACTGTAAACTATT 679
 Db 181 GlySerAsnAspArgValGlnGlnLysAlaIleSerGlnLeuGlnAspArgCysLysThrIle 200

Result No.	Score	Query Match	Length	DB	ID	Description
1	442	9.6	667	2	T09013	RING finger protein
2	436	9.5	667	2	T09482	ring finger protein
3	259	5.6	624	2	S28418	probable zinc-bind
4	253	5.5	551	2	JC7562	gliblactoma RING
5	253	5.5	609	2	A43966	nuclear phosphopro
6	246.5	5.3	792	2	T00088	hypothetical prote
7	224	4.9	518	2	JC7387	testis-abundant fi
8	223.5	4.8	574	2	S28275	hypothetical prote
9	223.5	4.8	974	2	E88549	protein F54G8.4 f
10	220.5	4.8	365	2	A30811	regulatory protein
11	212	4.6	477	2	JE0343	terf protein - rat
12	211.5	4.6	506	2	S37583	RING finger protein
13	208	4.5	801	4	TVHURE	transforming prote
14	207.5	4.5	513	1	TVHURF	ret finger protein

15	206	4.5	475	1	A37241	52K autocantigen Ro
16	205.5	4.5	442	2	A57041	transcription regu
17	204	4.4	630	2	A49656	estrogen-responsiv
18	200.5	4.3	1234	2	T00363	hypothetical prote
19	200	4.3	634	2	I49642	estrogen-responsiv
20	189	4.1	375	2	F88947	protein C39f7.2 [i
21	189	4.1	375	2	T33778	hypothetical prote
22	187.5	4.1	892	2	T09071	SH3 domain-contai
23	187	4.1	676	2	TC9222	77K muscle-derived
24	186.5	4.0	698	2	T32840	hypothetical prote
25	179.5	3.9	2346	2	T33829	Tpr homolog - finl
26	177	3.8	1051	2	S55259	tif1 protein - mou
27	174.5	3.8	662	2	T18323	probable transcrip
28	172.5	3.7	574	2	A46054	GMP-binding protei
29	171.5	3.7	412	2	D68072	protein zk1240.1 [
30	171.5	3.7	955	4	C40045	probable transcrip
31	169.5	3.7	775	2	D86261	hypothetical prote
32	169	3.7	1110	1	I51116	NF-180 - sea lamp
33	165	3.6	1020	1	QF7UH	neurofilament trip
34	164	3.6	802	2	S42518	PMU protein, splic
35	164	3.6	802	2	S44382	PMU protein, splic
36	162.5	3.5	3507	2	T34513	hypothetical prote
37	161	3.5	1222	2	T15689	hypothetical prote
38	159.5	3.5	2524	2	T18378	variant-specific s
39	158.5	3.4	633	2	S19244	gene WY1 protein -
40	158.5	3.4	860	2	S44380	PMU protein, splic
41	158.5	3.4	860	2	S42516	PMU protein, splic
42	158.5	3.4	906	2	T00039	hypothetical prote
43	157.5	3.4	292	2	T32000	hypothetical prote
44	157.5	3.4	589	2	S42517	PMU protein, splic
45	157.5	3.4	641	2	A40045	probable transcrip

ALIGNMENTS

[illegible]

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Db 21 ---LeuLeuLeuProCysAlaHisSerLeuCysPheAsnCysValAlaHisArg11LeuVal 39
Qy 248 -----GCCTAACCCGGTACTTACCACAAGAGAGGACCCAGCGGATCAGAGG 298
Db 40 SerHisCysAlaThrAsn-----GluProValGluSer11Le 51
Qy 299 GAGCGCTTCGCGTCTCCCTCTGACAGATGAGTGTGTAGACAGACATGGGGTCTTAT 358
Db 52 AsnAlaPheGlnCysProThrCysArgHisVal11LeuLeuSerGlnArg11LeuAsp 71
Qy 359 GGATCGCAGAGAAACCTGCTGCGTGAAGAAACATTTATGATCTACAGACAGAAATCC--- 415
Db 72 GlyLeuLysArgAsnVal11LeuGln11Asn11LeuAspArgPheGlnLysAlaSerVal 91
Qy 415 ----- 415
Db 92 SerGlyProAsnSerProSerGluThrArgArgGluArgAlaPheAspAlaAsnThrMet 111
Qy 415 ----- 415
Db 112 SerSerAlaGluLysValLeuCysGlnPheCysAspGlnAspProAlaGlnAspAlaVal 131
Qy 416 -----ACCAAGGCCA 424
Db 132 LysThrCysVal11ThrCysGlnValSerTyrCysAspGlnCysLeuLysAlaThrHisPro 151
Qy 425 GAAAAA-----TTGACCCAGCCCATG----- 448
Db 152 AsnLysLysProPheThrGlyHisArgLeu11GluPro11LeuProAspSerHis11LeuArg 171
Qy 449 -----TGTGAAGACATGAGAGAGAGACGCATCAACATCTATTGTCTGAACGTGAA 499
Db 172 GlyLeuThrCysLeuGlnHisGluAspGluLysValAsnMetTyrCysVal11ThrAspAsp 191
Qy 500 GTGCGCCACCTTCTCTGTCGAAGGTTTGGCGCCCAAGAGACTGCGACAGTGGCTCC 559
Db 192 GlnLeu11LeuCysAlaLeuCysLysLeuVal11GlyArgHisArgAspHisGlnValAla11 211
Qy 560 CTGACTCATGTGTTCCAGAGGACAGAGTCAAGAGTCAAGTATGATGATGCTGTACTTGTG 619
Db 212 LeuSerGlnArgTyrArgLysLeuLysGlnAsnLeuGlnSerAsnLeuThrAsnLeu11Le 231
Qy 620 GGAAGCAACATAGACTCAGAGGTGTGATCAGCCAGCTGAGAGACCTGTAAAACTATT 679
Db 232 LysArgAsnThrGluLeuGlu11ThrLeuLeu11AlaLysLeu11Gln11ThrCysGlnHisVal 251
Qy 680 GAGAGTCTCTCGAAGAAAGAAACAGACCTGTCTGGAATTTGATCAGCTTATACGC 739
Db 252 GluValAlaAsnAlaSerArgGlnGln11AlaLysLeuThrGluLysAspLeuLeu11Gln 271
Qy 740 ATCTGTGAGAGAGAGAAAGTGAATGACCAAGGCATC---ACTCGAAGACAGAGAG 796
Db 272 Ile11GlnGln11ArgArg-----Gln11Leu11GlyThrLys11LeuGlnGlu 287
Qy 797 AAATCTGAACATGTCGAACTCTTATCAGAGAAATTCGAT-----CACCTGAG 847
Db 288 LysVal11LeuArgLeuArgLysLeuAlaGlnGln11LeuAlaAsnCysLysGlnCysLeuGln 307
Qy 848 AACGATTCAGATTGCTGAGATCAGAGATCCAGTTCAATGATGAGCCCGAAATGCGACTA 907
Db 308 ArgSerAlaSerLeu11LeuSerGlnAlaGlnHisSerLeuLysGlnLysAsnAspHisAlaArg 327
Qy 908 TTTCTGAGAAATGCCAAGACCTGTGTGCAAAAGATCGTGAAGCATCAAGAGCGTTTACG 967
Db 328 PheLeuGlnThrAlaValAsn11LeuThrGluArgValSerMetAlaThrAlaSerSerGln 347
Qy 968 ATGGAGAAACTAGAACAAAGTTAT--GAGATCATGAGCAACTTCATGTCATTCAT 1024
Db 348 ValLeu11LeuProGlu11LeuAsnLeuAsnAspThrPheAspThrPheAlaLeuAspPheSer 367
Qy 1025 AGAGAGAAATAATTATCCGGAATTCATTT-----TCT 1060
Db 368 ArgGluLysLysLeuLeuGluCysLeuAspTyrLeuThrAlaProAsnProProAla11Le 387

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Qy 1061 AGAGAGAGAGAGAGAGAGAGATGACAGAGAAATATGATGAGAGAGAGAGAT 1120
Db 388 ArgGlnGluLeuLeuCysThrAlaSerTyrAspThr11LeuThrValHis11TrpThrSerGluAsp 407
Qy 1121 GCAGTAGAAGTA-----GAGAGCGCAAAAT 1147
Db 408 GluPheSerVal11AspTyrGlnLeuGln11Thr11LeuPheThrGlnAlaAsnVal 427
Qy 1148 GTTCAATATACATCTTCAGCGGAAG-- 1174
Db 428 ValSerLeuCysAsnSerAlaAspSerTyrMet11LeuAlaProAsn11LeuLysGlnAsnHis 447
Qy 1175 -----GAGAGCTGAG 1186
Db 448 TyrThrValHisGlyLeuGlnSerGlyThrLysTyr11LeuPheThrValLysAla11LeuAsn 467
Qy 1187 AAAGCTGACAGACCCCTCTCAGCTTCCCGACAGCTTCAGGTCCGCCAGAGCACTA-- 1243
Db 468 GlnAlaGlySerArgSerSerGluProGlyLysLeuLysThrAsnSerGlnProPheArg 487
Qy 1244 -----CTGCTTCC 1252
Db 488 LeuAspProLysSerAlaHisArgLysLeuLysValSerHisAspAsnLeuThrValGln 507
Qy 1253 -----TCTCAGAACCGTTTCA 1273
Db 508 ArgAspGluSerSerLysLysSerHisAlaProGluArgPheAlaGlnGlnLysSer 527
Qy 1274 ATGCCACCTGCTCAGATGCTCTGTGACACAGAGG-----GAGGTGTGCCC 1321
Db 528 TyrGlyValAlaGlnAsnVal11Phe11LeuAspSerGlyArgHisTyrTyrTrpGluVal11Thr 547
Qy 1322 ATTGGCTCT-----CAGCAGACCAACAGCTGAACT 1354
Db 548 SerGlySerThrTyrTrpAla11LeuGlyLeuAlaTyrArgSerAlaProLysHisGluTyr 567
Qy 1355 TCAGGCCCTTCAGAGCGGAAAGTGCAGATCCCTGTGTTTAACTAGTTAGTAAAGGC 1414
Db 568 IleGlyLysAsnAla11AspSerTrpAlaLeuCysArgCysHisAsnHis11TrpAlaValArg 587
Qy 1415 CAAGCCGAAACACAGCTCCAAACCACTTCGACATCATGAGAGTGAAGCTGGGTCAA 1474
Db 588 HisAspGlyLysGluThrPro11LeuAlaProAlaProHis-----LeuArgArg 603
Qy 1475 ATAGGCGCTCTG 1486
Db 604 ValGlyValLeu 607

RESULT 2
T09482
ring finger protein FX1 - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence revision 16-Jul-1999 #text change 09-Jul-2004
C:Accession: T09482
R:Periy, V.; Feather, S.; Smith, A.; Palmer, S.; Ashworth, A.
submitted to the EMBL data library, November 1997
A:Description: The human FX1 maps to chromosome Xp22.3: Implications for evolution of the
A:Reference number: Z16687
A:Accession: T09482
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-667 <PER>
A:Cross-references: UNIPROT:O15344; EMBL:AF035360; NID:g2827993; P1D:g2827994
C:Genetic8:
A:Gene: FX1
A:Map position: Xp22.3
A:Superfamily: rfp transforming protein
F:6-65/Domain: RING finger homology <RNM>

Alignment Scores:
Pred. No.: 6.5e-21 Length: 667
Score: 436.00 Matches: 146

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 15, 2005, 02:24:18 ; Search time 235 Seconds
(without alignments)
11287.533 Million cell updates/sec

Title: US-10-775-627A-3
Perfect score: 4611
Sequence: 1 cccgagattaccctacag.....ctcccttctcttctctcc 2590

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODE=frame+n2p.model -DEV=xlp
-O=/cgr2.1/USPTO.spool.p/US1075627/runat.14062005.140909.19280/app.query.faeta_1.2759
-DB=uniprot_03 -QFMT=faetan -SUFFIX=rup -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=20 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US1075627 @CGN 1.1 253 @runat.14062005.140909.19280 -NCPV=6 -ICPV=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2346.5	50.9	548	2	Q96DV2
2	2285.5	49.6	532	2	Q9BYV5
3	2232.5	48.4	540	2	Q81UD9
4	1909.5	41.4	452	2	Q96DV3
5	1848.5	40.1	436	1	RN29_HUMAN
6	1239.5	26.9	360	2	Q6INV6
7	1226	26.6	443	2	Q6DHSO
8	1162	25.2	366	2	Q9ERP3
9	1161	25.2	225	2	Q9GMX4
10	1154	25.0	342	2	Q9BYV3
11	1126	24.4	384	2	Q9BYV2
12	1121	24.3	351	2	Q91Z63
13	1088.5	23.6	353	1	RN28_HUMAN
14	1077	23.4	346	1	Q6NR77
15	1063	23.1	241	2	Q81UE4
16	1059	23.0	197	2	Q8C6Y1

17	1034.5	22.4	356	2	Q6DE39	Q6DE39 xenopus lae
18	934.5	20.3	429	2	Q6DC78	Q6DC78 brachydanio
19	910.5	19.7	345	2	Q6IOH8	Q6IOH8 brachydanio
20	861.5	18.7	348	2	Q7ZKH0	Q7ZKH0 brachydanio
21	470.5	10.2	151	2	Q8BWC4	Q8BWC4 mus musculus
22	467.5	10.1	729	2	Q7TMM1	Q7TMM1 mus musculus
23	465	10.1	728	2	Q9NQ86	Q9NQ86 homo sapien
24	459.5	10.0	733	2	Q6NU77	Q6NU77 xenopus lae
25	458	9.9	693	2	Q6PH04	Q6PH04 mus musculus
26	440.5	9.6	729	2	Q80MG7	Q80MG7 mus musculus
27	440	9.5	667	1	MID1_RAT	MID1_RAT
28	439.5	9.5	680	2	MID1_MOUSE	MID1_MOUSE
29	437.5	9.5	667	2	Q90WD1	Q90WD1 gallus gall
30	437	9.5	668	2	Q6DEU6	Q6DEU6 xenopus tro
31	436	9.5	667	1	MID1_HUMAN	MID1_HUMAN
32	433.5	9.4	667	2	Q7IR46	Q7IR46 gallus gall
33	431	9.3	685	1	MID2_MOUSE	MID2_MOUSE
34	431	9.3	685	2	Q6GX19	Q6GX19 mus musculus
35	431	9.3	685	2	Q6GX20	Q6GX20 cercopithec
36	431	9.3	715	1	MID2_HUMAN	MID2_HUMAN
37	431	9.3	715	2	Q6GX21	Q6GX21 cercopithec
38	430	9.3	667	1	MID1_MOUSE	MID1_MOUSE
39	423.5	9.2	759	2	Q7TMM2	Q7TMM2 mus musculus
40	421	9.1	441	2	Q641M2	Q641M2 mus musculus
41	420	9.1	524	2	Q6ZRL7	Q6ZRL7 mus sapien
42	414.5	9.0	424	2	Q6PL19	Q6PL19 mus sapien
43	414	9.0	498	2	Q6NT17	Q6NT17 homo sapien
44	413	9.0	551	2	Q9HSF2	Q9HSF2 homo sapien
45	413	9.0	759	2	Q7Z4K8	Q7Z4K8 homo sapien

ALIGNMENTS

RESULT 1
ID Q96DV2 PRELIMINARY; PRT; 548 AA.
AC Q96DV2;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE RING finger protein 29.
GN Name=RNFP29;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cardiac muscle;
RA Iakovenko A., Gautel M.,
RT "Titin-associated zinc-finger proteins link titin kinase to
transcriptional control."
RL J. Muscle Res. Cell Motil. 21:833-833(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cardiac muscle;
RX MEDLINE=22302063; PubMed=12414993;
RA Pizon V., Iakovenko A., Van der Ven P.F.M., Kelly R.A., Fattu C.,
RA Furst D.O., Karsenti B., Gautel M.,
RT "Transient association of titin and myosin with microtubules in
nascent myofibrils directed by the MURF2 RING-finger protein."
RL J. Cell Sci. 115:4469-4482(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Cardiac muscle;
RA Gautel M.S.,
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; A0243489; CAC43020.1; -!
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.

DR InterPro; IPR000315; Znf_Box.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00643; zf-B_box; 1.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00336; BBOX; 1.
 DR SMART; SM0184; RING; 1.
 DR PROSITE; PS00119; ZF_BOX; 1.
 DR PROSITE; PS00518; ZF_RING; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Metal-binding; Zinc; zinc-finger.
 SQ SEQUENCE 548 AA; 60465 MW; D7AB530A359FD67D CRC64;

Alignment Scores:

Score:	1.77e-130	Length:	548
Percent Similarity:	2346.50	Matches:	463
Best Local Similarity:	90.20%	Conservative:	34
Query Match:	50.89%	Mismatches:	46
DB:	2	Indels:	9
		Gaps:	3

US-10-775-627A-3 (1-2590) x Q96DV2 (1-548)

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QY 80 ATGAGCACTTCTGGAATTACAGCTTCTCCAAAGAGCAGACGACCATGATTAATTG 139
DB 1 Metseralaserleuamrlylserserpheserlysglulglnththmetaspasnu 20
QY 140 GAAAGCAACTGATCTGTCCATCTGCTTAGAGATGTTCAAGAAAGCTGTGATTTCTC 199
DB 21 Glulysglulnleuilecyeproilecyalsenulmetphenrlysprowalvalilleu 40
QY 200 CCTTGGCCAGCAACCTGTGCAAGAAATGTGCCAGTGCATCTTTCAGGCTTCAACCG 259
DB 41 ProcsygslnhisasnuCysarglyeCysalaseraspillepneglinalaserasnp 60
QY 260 TACTTACCACCAAGAGAGGAGCACACCGTGCATCAGGGGGCGCTTCGCTGCCCTCC 319
DB 61 TyrleupromrtharglygllythrthwetalaserlygllyargpneargCysproser 80
QY 320 TGCAGACATGAGTGGTGTAGACAGACATGGGGTCTATGAGACTGCAGAGAACCTGCTC 379
DB 81 CysarhsglsuValValleuasparghiseglyVallyrglyleuglnarhspasnu 100
QY 380 GTGAAAACATTATTTGATATCTCAAGCAGAAATCCACAGGCCCAAGAAAAAATTGAC 439
DB 101 Valalysnilleileaspilletyrlysglulglnserthrargproglulylaserasp 120
QY 440 CAGCCCATGTGTGAAGAGCATGAGAGGAGGACATCAATCTATTGTCTGAACCTTGAA 499
DB 121 GlnprometCysglulglnhlsiglulglnlualrgilleasnilletyrCysleuasncysglu 140
QY 500 GTGGCCACCTGTCTTCTGTGCAAGGTTTTTGCGCCCATTAAGACCTGCCAGTGGCTCC 559
DB 141 ValProthrCysserleucyelyelValphegylalhsilyBabpCysglinValAlaPro 160
QY 560 CTGACTCATGTGTTCACAGGCGACAGAGTCAAGCTCAAGTATGGTATTGCTGTGACTTGG 619
DB 161 leuthrhlsvalipheglnarlglnlysergluleuseraspGlyllealileleval 180
QY 620 GGAAGCAACGATAGAGTCCAGGGTGTGATCCAGCGCTGAGGAGCACTGTAAAACTATT 679
DB 181 GlyserasnpargvalGlnGlyValIleserlglnleuglnuaspThmCyslysthrIle 200
QY 680 GAGAGTGTCTGCAGAAAGCAGAAACAGGACCTGTGTGGAATTTGATCACTTATACGGC 739
DB 201 GluluglucysCysarglysglulglnleuglnleucysglulyspneaspTyleutrygly 220
QY 740 ATCTCGAAGAGAGAGAGACTGAATGACCCAGCCATCACTCGAACACAGAGAGAGAA 799
DB 221 IleuuglulglnarglysasnglulmetthrGlnValIlethrargThnglulglnlys 240
QY 800 CTGGAACATGTCCGAACTCTTATCAGAAAGTATCCGATCCGATCCGAGAGAACTTCCAG 859
DB 241 leuGlnhlsvalargAlaLeuilelylsystryserasphtsleuglnuasvalserlys 260

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QY 860 TTGGTGAAGTCAGGAATCCAGTTCAATGATGAGCCCAAAATGCGAGTATTTTCAGAAAT 919
DB 261 leuValglulserglylelglnpneMetaspGluProglulmetAlaValPheleuglnasn 280
QY 920 GCCAAGACCTGTGTCAAAAGATCGTGGAAGATCAAAAGCGCTTTCAGATGAGAACTA 979
DB 281 AlalserthrleuLeuylslyIleserGlnalaserlysalapheglnmetGlnlysIle 300
QY 980 GAACAAAGTTATGATTCAGACCACTTCACGTGCAATCTCAATAGAGAAAAAATT 1039
DB 301 GlulhlselytyrglulmetlaenhsphethrValasnleuasnargGlnGlnlysIle 320
QY 1040 ATCCGTGAATTTGACTTTTCTTAGAAGAGAGAGAGAAAGAT-----GCA 1087
DB 321 IleargglulileaspheptryrargGluaspGluaspGluaspGlnuglnuglnugln 340
QY 1088 GAGAGAAATGATGAAAGAGAGAA--GAGAGAGATCCAGTGAAGTGAAGAGGACGAA 1144
DB 341 GlyglulysglulglnuglnuglnuglnValGlygllyGlnlavalalGlnValGln 360
QY 1145 AATGTTCAATAGCATTTTCAAGGGGAAAGAGAGAGTCTGGAAGAGCTGAGAGCCCTCT 1204
DB 361 AsnValGlnthrGlnphepProgllyGluaspGluaspProglulysalaserGlnleuser 380
QY 1205 CAGCTTCCCGCAGAGCTTCAGGTGCGCCCGAGAGCCATCACTGCTCTTCCAGAACCG 1264
DB 381 Glnval-----GluenuglnAlaIalaproGlyAlaleuProvalaserProgluPro 398
QY 1265 TTTTCATTCATGCCACTGCTGCAAGATGTCCTGTGTGACACAGGGGAGGTGGCCATT 1324
DB 399 ProProAlaleuProProAlaIalaspAlaProvalthrGlnGlnGlnValIalProthr 418
QY 1325 GGCTCTCAGAGACCAACAGAGTCTGAAACTTCAGGCGCTTCAGAGGCGGAAATCGGGAT 1384
DB 419 GlyserglulglnthrGlnserGlnthrProvalProAlaIalaspGlnthrAlasp 438
QY 1385 CCTTGTGTTTAACTTACTAGTTGATTAAGGCAAAAGCCGGAACCAAGCTCCAAACCACT 1444
DB 439 ProleuphetrProserTprlyrlysglyGlnthrargysalathrThrAnProPro 458
QY 1445 TGCATCATGGAGATGAAGGTCTGGGTCAAATAGGGCTCTGGGCAATTGAGATTCAGT 1504
DB 459 CysthrProgllyserglulglnuglnleGlyProProgllyserGlnuaspSerasn 478
QY 1505 GTGAGTCGCGCAGAGAGTGCGAAGAGCCGCAACCAATGACAGGACGAGAGGAGTGAAG 1564
DB 479 ValargylsalaglnValAlaIalalalalalaserGlnargAlaIalalaserGlylys 498
QY 1565 GAGTCTAGTTCAACTGACAGCTACTCTCAAGATTGATTTGAGGCCCTTCTCCCAAGGA 1624
DB 499 GluthserAlarProAlaIalathrserGlnIleGlyPheGlnAlaProProleuglnGly 518
QY 1625 CAGTCTGCAAGCTTGGGAGATGGGGGTGGGT-GATCTGAGCCAGCTGCCACGTCTTC 1683
DB 519 GlnAlaIalalalProAlaIaserGlyserGlyAlaIaspserGlnProAlaIarghlsIlePhe 538
QY 1684 TCCCTTCTCGTGTGGAATCCCTAAATGAA 1714
DB 539 SerPheSerThr-LeuasnSerleuasngln 548

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RESULT 2

Q9BYV5 PRELIMINARY; PRT; 532 AA.
 ID Q9BYV5
 AC Q9BYV5
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE Ring finger protein 29.
 GN Name=BNP29;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=21140140; PubMed=11243782; DOI=10.1006/jmbi.2001.4448;
 RA Center T., Yano J., Kimura E., McElhinny A.S., Peilin K., Mite C.C.,
 RA Bang M.W., Trombikas K., Granzler H., Gregorio C.C., Sotiriachi H.,
 RA Labelt S.;
 RT "Identification of muscle specific ring finger proteins as potential
 RT regulators of the titin kinase domain.";
 RL J. Mol. Biol. 306:717-726(2001).
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 DR EMBL; AJ291712; CAC32840.1; -;
 DR GO; GO:0005874; C:microtubule; NAS.
 DR GO; GO:0004871; F:signal transducer activity; NAS.
 DR GO; GO:0007165; P:signal transduction; NAS.
 DR InterPro; IPR00315; Znf_Box.
 DR InterPro; IPR001841; Znf_Ring.
 DR Pfam; PF00643; ZF-B_Box; 1.
 DR Pfam; PF00097; ZF-C3HC4; 1.
 DR SMART; SM00336; BBOX; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS00119; ZF_BOX; 1.
 DR PROSITE; PS00518; ZF_RING_1; 1.
 DR PROSITE; PS0089; ZF_RING_2; 1.
 DR Metal-binding; Zinc; Zinc-finger.
 KW SEQUENCE 532 AA; 58634 MW; 8F12BAD35558952 CRC64;

Alignment Scores:

Pred. No.: 7.14e-127 Length: 532
 Score: 2285.50 Matches: 450
 Percent Similarity: 90.47% Conservative: 34
 Best Local Similarity: 84.11% Mismatches: 43
 Query Match: 49.57% Indels: 9
 DB: 2 Gaps: 3

US-10-775-627A-3 (1-2530) x Q9BYV5 (1-532)

QY 128 ATGGAAATCTGGAAAGCAAGATCTGCCATCTGCTAGAGATGTTCAAGAGCT 187
 Db 1 MetAspAsnLeuValGlnLeuIleCysProIleCysLeuGlnIleCysPheThrIleValPro 20
 QY 188 GTGGATATCTCCCTTCCAGACAACTGTGCAGGAATGTCACATGATCTTCCAG 247
 Db 21 ValValIleLeuProCysGlnIleAsnLeuCysArgIleCysAlaSerPheIlePheGln 40
 QY 248 GCCTTACCCGCTTACCTTACCCACAAAGAGAGCAACCGTGCATCAGGGGCGCTTC 307
 Db 41 AlaSerAsnProIleProIleProIleArgGlyGlyThrThrMetAlaSerGlyIleArgPhe 60
 QY 308 CGCTGTCCTCCCTGCGACACATGAGTGTGTTAGACAGACATGGGCTCTTGAAGTCCAG 367
 Db 61 ArgCysProSerCysArgIleGlnValIleAsnAspArgIleGlyValIleValIleGln 80
 QY 368 AGGAACCTGCTGTGGAAACATTTATGATATCTACAGAGAGGAAATCCACAGCCAGAA 427
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 QY 428 AAAAATGGACAGCCCATGTGTGAAGACATGAAGAGAGACATCAATCTATTGT 487
 Db 101 LysLysSerAspGlnProMetCysGlnGlnIleGlnGlnIleValIleAsnIleTyrCys 120
 QY 488 CTGAATCTGGAAGTCCCACTGTTCTTGTGCAAGTTTTGGCCCAATAGACTGC 547
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 QY 608 GCTGTACTTGTGGAGAACAGATGAGTCCAGGGTGTGATCAGCCAGTGAAGACACC 667
 Db 161 AlaIleLeuValGlySerAsnAspArgValGlnGlyValIleSerGlnLeuGlnAspThr 180

QY 668 TGTAAATCTATTGAGAGTGTGCAAGAAAGCAAGACCTGTGTGAATTTGAT 727
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 QY 848 AACGATCCAAATGTGGTGGAGTCAAGAAATCCAGTTATGATGAGCCCAATGCGAGTA 907
 Db 241 AsnValSerLysLeuValGlnIleSerGlyIleGlnPheMetAspGlnProIleMetAlaVal 260
 QY 908 TTTTGCAGATGCCAAGACCTGTTCAGAAAGATGTGGAAGCATCAAGCGCTTCAG 967
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 QY 1082 GATGCAAGAGAAATAGATGAGAGAGAGAGAG-----GATCAGTGAAGATA 1132
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 Db 379 SerProGlnProProProAlaLeuProProIleAlaAspAlaProValIleThrGlnIleGln 398
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 Db 399 ValIleProThrGlySerIleGlnIleThrThrGlnSerGlnThrProValIleAlaIleAla 418
 QY 1373 GAAACGCGGATCCCTGTTTACCTAGTGTGATTAAGGCCAAAGCCGAAACACAGC 1432
 Db 419 GlnThrAlaAspProLeuPheIleProSerThrTyrLysGlyGlnThrArgLysAlaThr 438
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 QY 1493 GAGATTCAGATGTGTCAGTCCGAGAGATGGGAGAAAGCCGCAACATAGACAGCGACA 1552
 Db 459 GlnAspSerAsnValArgLysAlaGlnValAlaAlaAlaIleAlaIleSerGlnIleArgAlaAla 478
 QY 1553 GTGAGTGTGAAGAGTCTAGTTCAACTGCACTGAGTACTCTCAGATTGATTGAGGCGCT 1612
 Db 479 ValSerGlyLysGlnIleSerAlaProAlaAlaIleSerGlnIleIleIlePheGlnIleAlaPro 498
 QY 1613 TCTCCCAAGGACAGTCTGTCAGCTTGGAGTGGGGGTGGGGT--GATCTGAGCCAGCT 1671
 Db 499 ProLeuGlnGlyGlnAlaIleAlaIleProAlaIleSerGlyAlaIleAspSerGlnProAla 518
 QY 1672 CGCCAGCTTCTCTCTCTCTGTTGAAATTCCTTAATGAA 1714
 Db 519 ArgGlnIlePheSerPheSerThr--LeuAsnSerLeuAsnGln 532

RESULT 3

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ID 081UD9 PRELIMINARY; PRT; 540 AA.
AC 081UD9;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE RING finger protein 29.
GN Name=RNFP29;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
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RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Iakovenko A., Gautel M.;
RT "Titin-associated zinc-finger proteins link titin kinase to
transcriptional control.";
RL J. Muscle Res. Cell Motil. 21:833-833(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=22302063; PubMed=12414993;
RA Pizon V., Iakovenko A., Van der Ven P.F.M., Kelly R.A., Fatu C.,
Furst D.O., Karentz E., Gautel M.;
RT "Transient association of titin and myosin with microtubules in
nascent myofibrils directed by the MURF2 RING-finger protein.";
RL J. Cell Sci. 115:4469-4482(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Gautel M.S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL: AJ431704; CAD24432.1; -
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR InterPro: IPR00315; Znf_Box.
DR InterPro: IPR01841; Znf_Box.
DR Pfam: PF00643; zf-B_box; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00336; BBOX; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS50119; ZF_BOX; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; zinc-finger.
SQ SEQUENCE 540 AA; 60245 MW; D16B7E706BF9C60A CRC64;

Alignment Scores:
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Score: 2232.50 Matches: 433
Percent Similarity: 91.18% Conservative: 32
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Query Match: 48.42% Indels: 7
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QY 140 GAAAGCAACATGATCTGTGCCATCTGCTAGAGATGTTCCAGAGACCTGTGTGCTATTC 199
DB 21 GluIysGlnLeuIleCysProIleCysLeuGlnMetPheThrIlyProValIleLeu 40
QY 200 CTTTGCAGCACAACCTGTGAGGAAATGTCCAGTGACATCTTCCAGGCTTAAACCG 259
DB 41 ProCysGlnIlnIAsnLeuCyArgIlyScyAlaSerAspIlePheGlnIlnIaSerAsnPro 60

QY 260 TACTTACCCACAAGAGGAGCCACCCTGTGGCATCAGGGGGCGGCTTCGCTCCCTCC 319
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QY 320 TGCAGCATAGGTTGGTTAGACAGCATGGGGTCTATGAGCTGGAGAGAACTGTCTC 379
DB 81 CyArgIlyGlnValIleuAspArgIlnsGlyValIlyToIyLeuGlnIlnArgAsnLeu 100
QY 380 GTGGAAAACATTATGATATCTACAAGCAGAAATCCACGAGCCAGAAAAAATTTGAC 439
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DB 161 LeuThrHisValPheGlnArgGlnLysSerGlnLeuSerAspIlyIleAlaIleLeuVal 180
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DB 181 GlySerAsnAspArgValGlnGlyValIleSerGlnLeuGlnAspThrCysLysThrIle 200
QY 680 GAGGAGTGTGCAAGAAACGAAACGAACTGTGTGAGAAATTTGATCACTTATCGGC 739
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QY 920 GCCAAGACCTGTGGCAAAAGATCGTAGAGCATCAAAAGCGCTTTCAGATGAGAAACTA 979
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QY 1205 CAGCTTCCCGCAGAGCTTCAGTCCGCCCGCAGACCACTACCTGCTTCCTCCAGAACCG 1264
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 15, 2005, 06:22:55 ; Search time 46 Seconds
(without alignments)
8406.134 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 1027090

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2809	60.9	545	US-09-908-988B-4	Sequence 4, Appli
2	1162	25.2	366	US-09-908-988B-2	Sequence 2, Appli
3	1088.5	23.6	353	US-09-484-970B-171	Sequence 121, App
4	1082	23.5	343	US-09-908-988B-6	Sequence 6, Appli
5	232.5	5.0	223	US-09-327-983-5	Sequence 5, Appli
6	228.5	5.0	539	US-09-949-016-6363	Sequence 6363, Ap
7	226.5	4.9	842	US-09-949-016-7012	Sequence 7012, Ap
8	226.5	4.9	870	US-09-949-016-9625	Sequence 9625, Ap
9	223.5	4.8	435	US-09-561-989-10	Sequence 10, Appl
10	223	4.8	519	US-09-949-016-7883	Sequence 7883, Ap
11	216.5	4.7	413	US-09-663-600A-198	Sequence 198, App
12	213.5	4.6	513	US-09-949-016-10972	Sequence 10972, A

13	207	4.5	487	2	US-08-724-394A-7	Sequence 7, Appli
14	206	4.5	475	4	US-09-949-016-6317	Sequence 6317, Ap
15	206	4.5	487	4	US-09-949-016-11205	Sequence 11205, A
16	204	4.4	643	4	US-09-949-016-10023	Sequence 10023, A
17	199.5	4.3	327	4	US-09-949-016-7575	Sequence 7575, Ap
18	199	4.3	835	4	US-09-949-016-9685	Sequence 9685, Ap
19	194	4.2	447	4	US-09-949-016-7884	Sequence 7884, Ap
20	187	4.1	218	4	US-09-327-983-6	Sequence 6, Appli
21	183.5	4.0	485	2	US-08-724-394A-8	Sequence 8, Appli
22	174	3.8	1155	4	US-09-949-016-10125	Sequence 10125, A
23	174	3.8	1155	4	US-09-949-016-10126	Sequence 10126, A
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25	172.5	3.7	574	1	US-08-049-473-2	Sequence 2, Appli
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33	168	3.6	703	3	US-08-910-925-4	Sequence 4, Appli
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35	164.5	3.5	158	4	US-09-663-600A-104	Sequence 104, App
36	163.5	3.5	664	4	US-09-949-016-9437	Sequence 9437, Ap
37	163	3.5	1162	2	US-08-728-323A-2	Sequence 2, Appli
38	163	3.5	1162	3	US-09-298-568-2	Sequence 2, Appli
39	163	3.5	1162	4	US-09-410-399-2	Sequence 2, Appli
40	163	3.5	1162	4	US-09-894-273-2	Sequence 2, Appli
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42	159	3.4	740	3	US-09-022-983-5	Sequence 5, Appli
43	159	3.4	742	4	US-09-949-016-11569	Sequence 11569, A
44	158.5	3.4	633	4	US-09-949-016-6259	Sequence 6259, Ap
45	158.5	3.4	680	4	US-09-949-016-10770	Sequence 10770, A

ALIGNMENTS

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RESULT 1
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; Sequence 4, Application US/09908988B
; Patent No. 6740751
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; FILE REFERENCE: MYOG:028US
; CURRENT APPLICATION NUMBER: US/09/908, 988B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/219, 020
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-908-988B-4

Alignment Scores:
Pred. No.: 1,1e-255
Score: 2809.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 60.92%
DB: 4
Gaps: 0

US-10-775-627A-3 (1-2590) x US-09-908-988B-4 (1-545)
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Db 1 MetSerThrSerLeuAsnTyrIlySerPheSerIyGluGlnInhThrMetAspAsnLeu 20
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QY	200	CCTTGCCGACCAACACTGTGCAGAGAAATGTGCAGATGACATCTTCAGAGCCCTAAACCG	259
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QY	1460	GAAGGTCTGGGCTCAAAATAGGGCTCTGGGGCATTAAGATTTCACAGTGTGACATCGCAGAA	1519
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RESULT 2

US-09-908-988B-2
; Sequence 2, Application US/09908988B

; Patent No. 6740751

; GENERAL INFORMATION:

APPLICANT: OLSON, ERIC

APPLICANT: SPENCER, JEFFREY A.

TITLE OF INVENTION: METHODS AND COMPOSITIONS

1. TITLE OF INVENTION: IN STRIATED MUSCLE CELLS

FILE REFERENCE: MYOG:028US

CURRENT APPLICATION NUMBER: US/09/908,988B

CURRENT FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: 60/219.020

PRIOR FILING DATE: 2000-07-18

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patent In Ver 2.1

DOE NUMBER: 20080401 DOE ID NO: 20080401

LENGTH: 366

LENGTH: 300
TYPE: PBT

OPCANTEN: Mrs. MURPHY

ORGANISM: MUB MUSCULUS
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US-03-308-388B-2

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Alignment scores:

Pred. No.:

Score: 11

Percent Similarity: 76

Best Local Similarity: 61

Query Match: 25

DB: 4

US-10-775-627A-3 (1-2590)

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Db 1 MetAsnphethr

140 GAAAAGCCTG

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RESULT 3
 US-09-484-970B-171
 ; Sequence 171, Application US/09484970B

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; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 171
; LENGTH: 353
; TYPE: PR
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 3575519CD1 (GENE ID 247384)
US-09-484-970B-171

Alignment Scores:
Pred. No.: 1,26e-93 Length: 353
Score: 1088.50 Matches: 214
Percent Similarity: 72.19% Conservative: 56
Best Local Similarity: 57.22% Mismatches: 81
Query Match: 23.61% Indels: 23
DB: Gaps: 3

US-10-775-627a-3 (1-2590) x US-09-484-970B-171 (1-353)
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Qy      686 TGCTGCAGAAAGAGAGAGACCTGTGTGAGAAATTTGATGACCTTAATGCGCATCTCG 745
Db      201 AsnSerHisGlnValLysGlnGlnLysSerGlnLysPheAspThrLeuTyAlaIleleu 220

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 15, 2005, 08:08:44 ; Search time 692.5 Seconds

(without alignments)
2867.397 Million cell updates/sec

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Xgapop 6.0 , Xgapext 7.0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2809	60.9	545	16 US-10-775-649-4	Sequence 4, Appl1
3	2809	60.9	545	16 US-10-775-627-4	Sequence 4, Appl1
4	2359.5	51.2	548	15 US-10-104-047-2643	Sequence 2643, Ap
5	1922.5	41.7	452	15 US-10-104-047-2403	Sequence 2403, Ap
6	1922.5	41.7	452	16 US-10-473-574-8	Sequence 8, Appl1
7	1735.5	37.6	414	9 US-09-764-864-821	Sequence 821, App
8	1166	25.3	358	10 US-09-890-688-58	Sequence 58, Appl
9	1162	25.2	366	9 US-09-908-988B-2	Sequence 2, Appl1
10	1162	25.2	366	16 US-10-775-649-2	Sequence 2, Appl1
11	1162	25.2	366	16 US-10-775-627-2	Sequence 2, Appl1
12	1139.5	24.7	366	17 US-10-204-921-57	Sequence 57, Appl
13	1132.5	24.6	366	17 US-10-061-043A-37	Sequence 37, Appl
14	1132.5	24.6	366	15 US-10-060-634C-37	Sequence 37, Appl
15	1121	24.3	351	14 US-10-061-043A-21	Sequence 21, Appl
16	1121	24.3	351	14 US-10-061-043A-36	Sequence 36, Appl
17	1121	24.3	351	14 US-10-061-043A-45	Sequence 45, Appl
18	1121	24.3	351	14 US-10-061-043A-46	Sequence 46, Appl
19	1121	24.3	351	14 US-10-061-043A-47	Sequence 47, Appl
20	1121	24.3	351	15 US-10-060-634C-21	Sequence 21, Appl
21	1121	24.3	351	15 US-10-060-634C-36	Sequence 36, Appl
22	1121	24.3	351	15 US-10-060-634C-45	Sequence 45, Appl
23	1121	24.3	351	15 US-10-060-634C-46	Sequence 46, Appl
24	1121	24.3	351	15 US-10-060-634C-47	Sequence 47, Appl
25	1088.5	23.6	353	15 US-10-094-749-2861	Sequence 2861, Ap
26	1088.5	23.6	353	15 US-10-221-625-85	Sequence 85, Appl
27	1087.5	23.6	353	14 US-10-061-043A-48	Sequence 48, Appl
28	1087.5	23.6	353	15 US-10-060-634C-48	Sequence 48, Appl
29	1086	23.6	289	14 US-10-061-043A-39	Sequence 39, Appl
30	1086	23.6	289	14 US-10-060-634C-39	Sequence 39, Appl
31	1086	23.6	340	14 US-10-061-043A-23	Sequence 23, Appl
32	1086	23.6	340	15 US-10-060-634C-23	Sequence 23, Appl
33	1082.5	23.5	366	9 US-09-764-864-808	Sequence 808, App
34	1082	23.5	343	9 US-09-908-988B-6	Sequence 6, Appl1
35	1082	23.5	343	16 US-10-775-649-6	Sequence 6, Appl1
36	1082	23.5	343	16 US-10-775-627-6	Sequence 6, Appl1
37	1022	17.1	326	15 US-10-250-613-4	Sequence 4, Appl1
38	790	12.2	202	14 US-10-061-043A-33	Sequence 33, Appl
39	790	17.1	202	15 US-10-060-634C-33	Sequence 33, Appl
40	786	17.0	184	9 US-09-764-864-1280	Sequence 1280, Ap
41	634.5	13.8	143	11 US-09-864-408A-6102	Sequence 6102, Ap
42	436	9.5	667	16 US-10-723-860-4278	Sequence 4278, Ap
43	432.5	9.4	552	16 US-10-408-765A-2368	Sequence 2368, Ap
44	405	8.8	736	15 US-10-108-260A-3552	Sequence 3552, Ap
45	387	8.4	122	9 US-09-764-864-1269	Sequence 1269, Ap

ALIGNMENTS

RESULT 1
US-09-908-988B-4
Sequence 4, Application US/09908988B
Patent No. US20020127690A1
GENERAL INFORMATION:
APPLICANT: OLSON, ERIC
APPLICANT: SPENCER, JEFFREY A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
FILE REFERENCE: MTCG:028US
CURRENT APPLICATION NUMBER: US/09/908, 988B
PRIORITY FILING DATE: 2000-07-18
PRIORITY APPLICATION NUMBER: 60/219, 020
PRIORITY FILING DATE: 2000-07-18
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 545
TYPE: PRT
ORGANISM: Mus musculus

US-09-908-988B-4

Alignment Scores:

Pred. No.: 3,45e-210
 Score: 2809.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 60.92%
 DB: 9

Length: 545
 Matches: 545
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-10-775-627a-3 (1-2590) x US-09-908-988B-4 (1-545)

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QY     140  GAAAGCAACTGATGTGCCATGTGCTAGAGATGTTCAAGAGCCGTGGTCAATTTC 199
DB      21  GluLysGlnLeuLleCysProLleCysLeuGlnMetPheThrLysProValLleLeu 40
QY     200  CCTTGCCAGACAACCTGTGAGAAATGTGCAGTGCATCTTCCAGCCCTTAACCCG 259
DB      41  ProCysGlnHleAsnLeuCysArgLysCysAlaSerAspLlePheGlnAlaSerAsnPro 60
QY     260  TACTTACCCACAAGAGAGGCAACCGTGGCATAGGGGGCGCTTCCGCTGTCCCTCC 319
DB      61  TyrLeuProThrArgGlyGlyThrThrValAlaSerGlyGlyArgPheArgCysProSer 80
QY     320  TGCAAGACATGAGGTGTGTAGACAGACATGAGGGGTCTATGAGCTGCAGAGAACCTGTC 379
DB      81  CysArgHleGlnValValLeuAspArgHleGlyValLleTyrGlyLeuGlnArgAsnLeu 100
QY     380  GTGAAAAATTATGATATATCTACAAGCAGAAATCACACAGGCCGAAAAAAATTGGAC 439
DB     101  ValGlnAsnLleLleAspLleTyrLysGlnGlnSerThrArgProGlnLysLeuAsp 120
QY     440  CAGCCCATGTGTGAAGACATGAAGAAGACGACATCTATTGTCTGAACTGTGAA 499
DB     121  GlnProMetCysGlnGlnHleGlnGlnLleAsnLleTyrCysLeuAsnCysGln 140
QY     500  GTGCCCACTGTCTTGTGCAAGGTTTGTGGCGCCATAAGAACTGCAGAGGTGGCTCC 559
DB     141  ValProHleCysSerLeuCysLysValAlaPheGlnAlaHleLysAspCysGlnValAlaPro 160
QY     560  CTGACTCATGTGTTCAGAGCAGAAAGTCAAGACTCAGTGAATGTGATTTGCTGTAATTGTG 619
DB     161  LeuThrHleValPheGlnArgGlnLysSerGlnLysSerAspGlyLleAlaValLeuVal 180
QY     620  GGAAGCAACGATAGAGTCCAGGGGTGTGATCAGCCAGCTGAGAGACCTGTAAAACTATT 679
DB     181  GlySerAsnAspArgValGlnGlyValLleSerGlnLeuGlnAspThrCysLysThrLle 200
QY     680  GAGAGTGTGTGAGAAAGCAGAAACAGAGCCGTGTGGAATTTGATCACCTTATTAAGGC 739
DB     201  GlnGlnLysCysArgLysGlnLysGlnLysPheCysGlnLysPheAspHleLeuTyrLle 220
QY     740  ATCTGTGAGAGAGAGAACTGAAATGACCCAGCCATCACTCGAAACAAGAGAGAGAAA 799
DB     221  IleLeuGlnGlnLysArgLysThrGlnMetThrGlnAlaLleThrArgThrGlnGlnLys 240
QY     800  CTGGAACATGTCCGAACCTTATACGAAAGTATTCGATCACCTGAGAGACGTATCCAG 859
DB     241  LeuGlnHleValArgThrLeuLleArgLysTyrSerAspHleLeuGlnAsnValSerLys 260
QY     860  TTGGTGAAGTCAAGAAATCCAGTTCATGATGAGCCGGAAGAGGAGTATTTCTGAGAT 919
DB     261  LeuValGlnSerGlyLleGlnPheMetAspGlnProGlnMetAlaValPheLeuGlnAsn 280
QY     920  GCCAAGACCTGTGCAAAAAGATCGTGAAGCATCAAAAGCGTTTCAGATGAGAGAACTA 979
DB     281  AlaLysThrLeuLeuGlnLysLleValGlnAlaSerLysAlaPheGlnMetGlnLysLeu 300
QY     980  GAAACAAGTATAGATCATGAGCAATTCACGTCAATTCATATAGAGAAAAAATT 1039

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DB     301  GlnGlnLleTyrGlnLleMetSerAsnPheThrValAsnLeuAsnArgGlnLysLle 320
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DB     321  IleArgGlnLleAspPheSerAspArgGlnGlnGlnGlnGlnLysPheArgGlnLleAsp 340
QY    1100  GAAAGAGAGAGAGAGATGACATGATGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 1159
DB     341  GlnGlnGlnLysGlnGlnGlnLysPheValGlnValGlnLysGlnLysValGlnLleAla 360
QY    1160  TCTTCAGGGGAAAGAGAGATCTGAGAGAAAGCTGCAGAGCCCTCAAGCTTCCCGAGAG 1219
DB     361  SerSerGlyGlnGlnGlnSerLeuGlnLysAlaAlaGlnProSerGlnLeuProAlaGln 380
QY    1220  CTTGAGGTCCGCCAGAGACCACTACCTGCTTCCCTCAGAAACGTTTTCATCCATGCCA 1279
DB     381  LeuGlnValAlaProGlnProLeuProAlaSerSerProGlnProPheSerSerMetPro 400
QY    1280  CTTGCTGACAGATGTCTGTGACACAGAGGAGGTGGTCCATTTGGCTTCAGACAGACC 1339
DB     401  ProAlaAlaAspValLeuValThrGlnGlyGlnValValProLleGlySerGlnThr 420
QY    1340  ACAAGTCTGAATCTTCAAGCCCTTGCAGAGCGGAAACCTGGATCCCTGTTTACCCT 1399
DB     421  ThrGlnSerGlnThrSerGlyProSerAlaAlaGlnThrAlaAspProLeuPheTyrPro 440
QY    1400  AGTTGTATATAAGGCCAAAGCCGAAAAACAGCTCCAAACCACTTGCATCTGAGGAGT 1459
DB     441  SerTyrTyrLysGlnGlnSerArgLysThrSerSerAsnProProCysThrHleGlySer 460
QY    1460  GAAAGTGTGGGTCAATAGGGGCTCTGGGCAATTGAGGATTCAGTGTGCAGTCCAGAA 1519
DB     461  GlnGlyLeuGlyGlnLleGlyProLeuGlyLleGlnAspSerSerValGlnSerAlaGln 480
QY    1520  GTGGCAAGAACCCCAACCATGAGCAGGCGCAGTGAAGTGTGAAGCTTAATTCAACT 1579
DB     481  ValAlaGlnAlaAlaThrAsnGlnGlnAlaAlaValSerGlyLysGlnSerSerThr 500
QY    1580  GCAGCTACCTCTCAGATTGTGATGAGGCCCTTCTCCAGAGGACAGTGCAGCCCTTG 1639
DB     501  AlaAlaThrSerGlnLleGlyPheGlnAlaProSerProGlnGlnSerAlaAlaLeu 520
QY    1640  GGAAGTGGGGGTGGGTGATCTGAGCCAGCTGCACGCTTCTCTCTGCTGTGGTGG 1699
DB     521  GlySerGlyGlyValLleLeuSerGlnLeuAlaThrSerSerProSerProGlyLeu 540
QY    1700  AATTCCCTTAATGAA 1714
DB     541  AsnSerLeuAsnGln 545

RESULT 2
US-10-775-649-4
; Sequence 4, Application US/10775649
; Publication No. US20040132160A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; FILE REFERENCE: MTG:0280SD2
; CURRENT APPLICATION NUMBER: US/10/775,649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 09/908,988
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Mus musculus

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US-10-775-649-4

Alignment Scores:

Pred. No.:	3,456-210	Length:	545
Score:	2809.00	Matches:	545
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	60.92%	Indels:	0
DB:	16	Gaps:	0

US-10-775-627A-3 (1-2590) x US-10-775-649-4 (1-545)

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QY 140 GAAAGCAAGTATCTGTCCCATCTGCGCTAGAGATGTTCAAGAACTGTGCTATTCCTC 199
Db 21 GluLysGlnLeuIleCysProIleCysLeuGlnMetPheThrLysProValIleLeu 40
QY 200 CTTTGCAGACAACTGTGCGAAGAAATGTCCGATGACATCTTCCAGGCTCTTAACCG 259
Db 41 ProCysGlnIleAsnLeuCysArgLysCysAlaSerAspIlePheGlnAlaSerAsnPro 60
QY 260 TACTTACCAACAAGAGGAGCACCAGCTGGCATCAGAGGAGCGCTCCGCTGTCCCTCC 319
Db 61 TyrLeuProThrArgLysGlyThrThrValAlaSerGlyAlaPheArgCysProSer 80
QY 320 TGCAGACATGAGGTGTAGACAGACATGGGGTCTATGAGACTGCAGAGAACTGCTC 379
Db 81 CysArgHisGlnValValLeuAspArgHisGlyValTyrGlyLeuGlnAlaGlnAsnLeu 100
QY 380 GTGAAAAAATTATGATATCTTACAGACAGAAATCCACAGGCGCAAAAAAATTGAC 439
Db 101 ValGlnAsnIleIleAspIleTyrLysGlnIleSerThrArgProGlnLysLeuAsp 120
QY 440 CAGCCCATGTGTGAAGCATGAAGAGAAAGCATCAACATCTATTGCTGAAGTGA 499
Db 121 GlnProMetCysGlnGlnIleGlnGlnIleGlnIleGlnIleTyrCysLeuAsnCysGln 140
QY 500 GTGCCCACTGTTCCTTGTGCAAGGTTTTTGGCGCCCATAGAGACTGCCAGTGGCTCC 559
Db 141 ValProThrCysSerLeuCysLysValPheGlyAlaHisLysAspCysGlnValAlaPro 160
QY 560 CTGACTCATGTGTTCCAGAGCAGACAGTCAAGCTCAGTGAATGATATTCCTGCTG 619
Db 161 LeuThrHisValPheGlnArgGlnLysSerGlnLeuSerAspGlyIleAlaValLeuVal 180
QY 620 GGAAGCAACGATAGTCCAGGGTGTGATCAGCGACGTCGAGGACACCTGTAAACTATT 679
Db 181 GlySerAsnAspArgValGlnGlyValIleSerGlnLeuGlnAspThrCysLysThrIle 200
QY 680 GAGAGTGTCTGAGAAAGAGAAACAGAGACTGTGTGAGAAATTTGATCACTTAAGGC 739
Db 201 GlnGlnCysCysArgLysGlnLysGlnAspLeuCysGlnLysPheAspHisLeuTyrGly 220
QY 740 ATCTTGAGAGAGAGAAAGTGAATGAATGACCAACCATCACTGCAACACAGAGAGAAA 799
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QY 800 CTGGAACATGTCGCAACTCTTATCAGGAAGATTCGATCCAGTCCGGAAGCTATCCAG 859
Db 241 LeuGlnHisValAlaGlnThrLeuIleArgLysTyrSerAspHisLeuGlnAsnValSerLys 260
QY 860 TTGGTGAGTCAAGAAATCAGTTTCATGATGAGCGCCGAATAGCAGTATTTCTCAGAAAT 919
Db 261 LeuValGlnSerGlyIleGlnPheMetAspLysProGlnMetAlaValPheLeuGlnAsn 280
QY 920 GCCAAGACCTCTGTTCCAAAAGATGTTGAACATCAAAAGGCTTTCAGATGGAAGAACTA 979
Db 281 AlaLysThrLeuLeuGlnLysIleValGlnAlaSerLysAlaPheGlnMetGlnLysLeu 300
QY 980 GAACAGAGTTATGAGATCATGAGCAACTTCACTGTCAATTCATCATAGAGAAAGAAATTT 1039
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QY 1040 ATCCGTAATTAATGACTTTCTAGAGAAAGAGAAAGAAAGAAATGATCAGAGAAATAGAT 1099
Db 321 IleArgGlnIleAspPheSerArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 340
QY 1100 GAAGAAGAGAAAGAGAGATGATGATGAGAAAGTGAAGAGAGAGAGAGAAATGTTCAATGCA 1159
Db 341 GlnGlnGlnIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 360
QY 1160 TCTTCAAGGAGAGAGAGAGATCTGAGAAAGCTGACAGAGCTTCTCAGCTTCCCGAGAG 1219
Db 361 SerSerGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 380
QY 1220 CTTTCAAGTGGCCCAAGACCACTACTCTCTCTCTCCAGAACCTTTTCAATCCAGACCA 1279
Db 381 LeuGlnValAlaProGlnLysProLeuProAlaSerSerProGlnProPheSerSerMetPro 400
QY 1280 CTTGCTGAGATGCTCGGTGACACAGAGGAGAGAGTGGTGGCTTCCATGCTTCCAGAGACC 1339
Db 401 ProAlaAlaAspValLeuValThrGlnGlyGlnValValProIleLysSerGlnGlnThr 420
QY 1340 ACAAGTCTGAACCTTCAAGCCCTTCAAGACCGGAAATCGGATCCCTTGTGTTTAACTT 1399
Db 421 ThrGlnSerGlnThrSerGlyProSerAlaAlaGlnThrAlaAspProLeuPheTyrPro 440
QY 1400 AGTTGGTATTAAGCCCAAGACCGGAAACCAAGCTCCCACTTGCATCTGAGAGT 1459
Db 441 SerTyrLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 460
QY 1460 GAAGTCTGGGTGAATTAAGGAGCTCTGGGCAATGAGAGATTCAGTGTGACAGTCCGAGAA 1519
Db 461 GlnGlyLeuGlyGlnIleGlyProLeuGlyIleGlnLysSerSerValGlnSerAlaGln 480
QY 1520 GTGCAGAAAGCCCAACCAATGAGCAGCAGCAGTGAAGTGAAGATGATTAACCT 1579
Db 481 ValAlaGlnAlaIleThrAsnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 500
QY 1580 GCAGCTACTCTGATGATGATGATGAGCCCTTCTTCCAGGAGACAGTCTGACGCTTG 1639
Db 501 AlaAlaThrSerGlnIleGlyPheGlnAlaProSerProGlnGlnGlnSerAlaAlaLeu 520
QY 1640 GGGAGTGGGGGTGGGGATCTGAGCAGCTGCCAGCTTCTCTGCTTCCGCTTGG 1699
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QY 1700 AATTCCCTAAATGAA 1714
Db 541 AsnSerLeuAsnGln 545

RESULT 3
US-10-775-627-4
: Sequence 4, Application US/10775627
: Publication No. US20040142446A1
: GENERAL INFORMATION:
: APPLICANT: OLSON, ERIC
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
: FILE REFERENCE: WMOG-028USD1
: CURRENT APPLICATION NUMBER: US/10/775,627
: PRIOR FILING DATE: 2004-02-10
: PRIOR APPLICATION NUMBER: 09/908,988
: PRIOR FILING DATE: 2001-07-18
: PRIOR APPLICATION NUMBER: 60/219,020
: NUMBER OF SEQ. ID NOS: 6
: SOFTWARE: PatentIn Ver. 2.1
: SEQ. ID NO. 4
: LENGTH: 545
: TYPE: PRT
: ORGANISM: Mus musculus
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US-10-775-627-4

Alignment Scores:

Pred. No.:	3,45e-210	Length:	545
Score:	2809.00	Matches:	545
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	60.92%	Indels:	0

US-10-775-627A-3 (1-2590) X US-10-775-627-4 (1-545)

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QY	140	GAAAGCAACATGATCTGTCCCATCGCTAGAGATGTTACAGAACCTGTGGTCAATTCTC	199
Db	21	GIuYsGInLeuIleCysProIleCysLeuGlnMetPheThrLysProValIleLeu	40
QY	200	CTTTGCCAGACAACCTGTGCAGGAATGTGCACATCTTCAGAGCCTTAACCCG	259
Db	41	ProCysGlnHisAsnLeuCysArgLysCysAlaSerAspIlePheGlnAlaSerAsnPro	60
QY	260	TACTTATCCCAAGAAGAGGAGCACCCGCTGGCATAGAGGGGCCCTTCGCTGTCCCTCC	319
Db	61	TyrLeuProThrArgLysGlyThrThrValAlaSerGlyGlyArgPheArgCysProSer	80
QY	320	TGCAGACATGAGTGTGTGTAGACAGACATGGGGGCTTATGGACCTGCAGAGAACCTGTGC	379
Db	81	CysArgHisGlnIuValIleLeuAspArgHisGlnValIleTyrGlyLeuGlnArgAsnLeu	100
QY	380	GTGGAAAAATTATTTATATCTTACAGCAGGAATCCACAGGCCAGAAAAAAATTGGAC	439
Db	101	ValGlnAsnIleIleAspIleTyrLysGlnGlnuSerThrArgProGlnLysLysLeuAsp	120
QY	440	CAGCCCATGTGTGAAGACATGAAGAAGAACGATCAACATCTATTGTCTGCATGTGAA	499
Db	121	GlnProMetCysGlnGlnHisGlnGlnIuArgIleAsnIleTyrCysLeuAsnCysGln	140
QY	500	GTGGCCACCTGTCTCTGTGCAGAGTTTGTGGCGCCCTTAAGGAATGGCAGAGTGGCTCC	559
Db	141	ValProThrCysSerLeuCysLysValIlePheGlyAlaHisLysAspCysGlnAlaLAspPro	160
QY	560	CTGACCTCATGTCTTCAGAGGCAGAAAGTACAGAGCTCACTGATGTGATTTCTGTACTTGTG	619
Db	161	LeuThrHisValPheGlnArgGlnLysSerGlnLeuSerAspArgGlyIleAlaValLeuVal	180
QY	620	GGAGCAACGATAGATCCAGGGGTGTATCAGCCAGCTGGAGACACCTGTAAACTAT	679
Db	181	GlySerAsnAspArgValGlnGlyAlaIleSerGlnLeuGlnAspThrCysLysThrIle	200
QY	680	GAGAGGTCTCCAGAAACAGAAACAGGACCTGTGTGAGAAATTGATCACCTATACGGC	739
Db	201	GlnGlnCysCysAspLysGlnLysGlnLysAsnLeuCysGlnLysPheAspHisLeuTyrGly	220
QY	740	ATCTGTGAGAGAGAGGAGACATGAATGAACCCAGGCATCACTCGAAACAGAGAGAGAA	799
Db	221	IleLeuGlnGlnIuArgLysThrGlnMetThrGlnAlaIleIleHisArgThrGlnIuGlnLys	240
QY	800	CTGGAACATGTCCGAACCTTATATCAGGAAGTATTCGATCACTTGAGAAACGTATCCAA	859
Db	241	LeuGlnHisValArgThrLeuIleIleArgLysTyrSerAspHisLeuGlnAsnValSerLys	260
QY	860	TTGGTGGAGTCAAGGAATCCAGTTCTATGATGAGGCCGAAATGGCAGTATTTCTGCAGAT	919
Db	261	LeuValGlnSerGlyIleGlnPheMetAspGluProGlnMetAlaValPheLeuGlnAsn	280
QY	920	GCCAAAGACCTCGTTGCAGAAAGATCGTGAAGACATCAAGGGCTTTCAGATGGAGAAACTA	979
Db	281	AlaLysThrLeuLeuGlnLysIleValGlnAlaSerLysAlaPheGlnMetCyluLysLeu	300
QY	980	GAAACAAGTTATGAGATCATGACGAACTTCACTGTCAATCTCCAAATGAGAGAAAGAAATT	1033

[illegible]

Score: 2359.50 Matches: 465
Percent Similarity: 90.56% Conservative: 34
Best Local Similarity: 84.39% Mismatches: 44
Query Match: 51.17% Indels: 9
DB: 15 Gaps: 3

US-10-775-627a-3 (1-2590) x US-10-104-047-2643 (1-548)

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QY 80 ATGAGCACTTCTGTAATTCAAGTCTTTCCAAAGAGAGAGACCATGATACTTG 139
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QY 140 GAAAGCAACTGATCTGTCCCATCTGCTAGAGATGTTTCAAGAGCCCTGTGCTCTC 199
DB 21 GlnYglGlnLeuLeuCySpProLeuCybLeuGlnMetPheThrLySProValIleLeu 40
QY 200 CTTTGCCAGACAACTCTGTCAGAGAAATGTGCCAGTGCATCTTCCAGGCTCTAACCCG 259
DB 41 ProCyGlnHisAsnLeuCybArgLyScyAlaSerAspIlePheGlnAlaSerAsnPro 60
QY 260 TACTTACCCCAAGAGAGGACCAACCGTGGCATCAGGGGGCGGCTTCGCTCCCTCC 319
DB 61 TyrLeuProThrArgLyGlnYrLThrMetAlaSerGlyGlyArgPheArgCySpProSer 80
QY 320 TGCAGACATGAGGTGGTGTAGACAGACATGGGGTCTATGACTGCAGAGAACTGTCTC 379
DB 81 CybArgHisGlnValValIleAsnAspArgHisGlyValIlyrGlyLeuGlnArgAsnLeu 100
QY 380 GTGGAAGAACTTATGATATCTCAAGACAGAAATCCACAGGCCCAAGAAAAAATTGGAC 439
DB 101 ValGlnAsnIleIleAspIleTyrLySglnGlnIleSerThrArgProGlnYlySerAsp 120
QY 440 CAGCCCATGTGTAAAGAGTGAAGAGAAACGATCAACATCTTATGTCTGAACCTGGA 499
DB 121 GlnProMetCySglnGlnIlySglnGlnIlyArgIleAsnIleTyrCySLeuAsnCySgln 140
QY 500 GTGCCACACTGTCTCTGTGCAAGGTTTTGGCGCCCATAGAGACTGCCAGTGGCTCC 559
DB 141 ValProThrCysSerLeuCySlyValPheGlyAlaHisIlyAspCySglnValAlaPro 160
QY 560 CTGACTCATGTGTCCAGAGGCAAGAACTCAGAGCTCAGTATGATGCTGTACTTGTG 619
DB 161 LeuThrHisValPheGlnArgGlnIlySerGlnLeuSerAspGlyIleAlaIleLeuVal 180
QY 620 GGAAGCAACGATAGAGTCCAGGCGGTGTGATGAGCCATGAGAGACCTGTAAACTAT 679
DB 181 GlySerAsnAspArgValGlnGlyValIleSerGlnLeuGlnAspThrCysLySThrIle 200
QY 680 GAGGAGTGTGCAGAAAGCAGAAACAGACCTGTGTGAGAAATTTGATCACTATACGGC 739
DB 201 GlnGlnCySArgLySglnIlySglnIlyLeuCySglnYlySPhesPlyrLeuYrGly 220
QY 740 ATCTTGAGAGAGAGAAAGTGAATGACCAACCATCACTCGAACACAGAGAGAGAA 799
DB 221 IleLeuGlnIlyArgLySAsnGlnMetThrGlnValIleThrArgThrGlnIlyGly 240
QY 800 CTGGAACATCTCGAACTCTTATCAGAAATATTCGATCACTCGAGAAACGATCCAG 859
DB 241 LeuGlnHisValIlyArgAlaLeuIleIlySlyrSerAspHisLeuGlnAsnValIleLyS 260
QY 860 TTGTTGAGTCCAGAAATCCAGTTCATGATGAGCCCAAGATGGCAGATTTCTGCAGAA 919
DB 261 LeuValGlnSerGlyIleGlnIlyPheMetAspGlnProGlnMetAlaValIlePheLeuGlnAsn 280
QY 920 GCCAAGACCTGTTCAGAAAGATGTGGAAGCATCAAGGCGTTTCAGATGAGAAACTA 979
DB 281 AlaIlySerThrLeuLeuYlySlyIleSerGlnAlaSerLySAlaPheGlnMetGlnYlyS 300
QY 980 GAACAGGTATATAGATCATGAGACATTCATGCTCAATCTCAATGAGAGAGAAATTT 1039
DB 301 GlnHisGlyIlyrGlnIlyAsnMetAsnHisPheThrValAsnIlyAsnArgGlnGlnYlyS 320
QY 1040 ATCCGTGAATATGACTTTTCTAGA-----GAAAGAGAAAGAGAAAGAAATGACAGAGAA 1093

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DB 321 IleArgGlnIleAspPheTyrArgGlnAspGlnAspGlnGlnIlyGlyGlyGln 340
QY 1094 ATAGAGTAAGAGAGAGAGAGAGAG-----GATGACGTGAGAACTAGAGAGAGAGAA 1144
DB 341 GlnYlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 360
QY 1145 AATGTTCAATAGACATCTTCAAGGGGAGAGAGAGAGTCTGAGAAAGCTGAGAGCCCTCT 1204
DB 361 AsnValGlnIlyThrGlnPheProGlnAspGlnAsnProGlnYlySAlaSerGlnLeuSer 380
QY 1205 CAGCTTCCCGCAGAGCTTCAAGTCCGCCCAAGACCACTACCTGCTTCTCTCCAGAACG 1264
DB 381 GlnVal-----GlnLeuGlnAlaIlyProGlnYlyAlaLeuProValSerSerProGlnPro 398
QY 1265 TTTTCATCATGCAACCTGCTCAGATGTCCTGTGTACACAGGGGGAGGTGGTCCATT 1324
DB 399 ProProAlaLeuProProAlaIlyAspAlaProValThrGlnGlnGlnValIlyValProThr 418
QY 1325 GGCTTCACAGACACACACAGCTGTGAACCTTCAAGGCGCTTCAAGAGCGGAACTCGCAT 1384
DB 419 GlySerGlnGlnIlyThrThrGlnSerGlnIlyThrProValProAlaIlyAlaIlyThrAlaAsp 438
QY 1385 CCCTTGTTTACCTTATGTTGTATAAAGGCCAAAGCCGAGAAACAGCTCCAACTCAACT 1444
DB 439 ProLeuPheTyrProSerTyrPyrLySglnGlnIlyThrArgYlyAlaIlyThrAsnProPro 458
QY 1445 TGCATCTCAGGAGTGAAGTCTGGGTCAATATAGGCGCTCTGGGCAATTGAGATTCACAG 1504
DB 459 CyThrProGlnIlySerIlyGlnIlyLeuGlnIlyGlnIlyProProGlnIlySerGlnIlySerAsn 478
QY 1505 GTGCAGTCCGCAAGATGGCAGAAAGCCGCAACCAATGAGACAGACAGTGAAGTGAAG 1564
DB 479 ValArgLyAlaGlnValAlaIlyAlaIlyAlaIlyAlaIlySerGlnArgAlaIlySerGlyLyS 498
QY 1565 GAGTCTAGTTCACATGCACTCACTCTCAGATTTGATTTGAGGCCCTTCTCCAGAGAA 1624
DB 499 GlnThrSerAlaProAlaIlyThrSerGlnIlyGlyPheGlnIlyAlaProProLeuGlnGly 518
QY 1625 CAGTCTGCAAGCTTGGGAGTGGGGGTGGGGT- GATCTCGAGGCACTGGCCACGTCTTC 1683
DB 519 GlnAlaIlyAlaIlyProAlaIlySerGlyAlaIlyAspSerGlnIlyProAlaIlyArgHisIlePhe 538
QY 1684 TCCTTCTCGTGTGAATTCCTTAATGAA 1714
DB 539 SerPheSerTyrLeuAsnSerLeuAsnGln 548

RESULT 5
US-10-104-047-2403
; Sequence 2403, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104, 047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2403
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2403

Alignment Scores:
Pred. No.: 5,1e-141 Length: 452
Score: 1922.50 Matches: 392
Percent Similarity: 75.14% Conservative: 22
Best Local Similarity: 71.14% Mismatches: 33
Query Match: 41.69% Indels: 105

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DB: 15 Gaps: 4
US-10-775-627a-3 (1-2590) x US-10-104-047-2403 (1-452)
OY ATGAGCACTTCTCGAATTACAGAGTCTTCTCCAAAGAGCAGACAGCATGATTAACCTTG 139
DB 1 Metceralaserleuentryrlyserpheserlysglungrlnthrmecaspmlneu 20
OY 140 GAAAGCAACTGATCTGTCCATCTGCTTAGAGATGTTCAAGAACTCTGGTCAATCTC 199
DB 21 GlulysgluleuileCyserProileCyserleuglmetPhethrlyspovalValileu 40
OY 200 CCTTGCCAGCAACCTGTGCAAGAAATGCGCACTGACATCTTCCAGGCTCTTAACCG 259
DB 41 ProCysgmihiasmlneuCyserglyserCysalaserapillepheglnalaseraspro 60
OY 260 TACTTACCACAAGAGAGGAGCACCAGTGGATAGAGGGGCGGTTCCGCTGCCCTCC 319
DB 61 TyreuprotmrarhrglyglythrThrmecalaserglylyArspheArxCysaroser 80
OY 320 TGCAGACATGAGGTGTGTAGACAGACATGGGGTCTATGAGCTGCAAGAGAACCTGCTC 379
DB 81 CysarhghsglulvalValleuaspahghisgllyvallyrgrlyleuglnarhspmlneu 100
OY 380 GTGAAAACATTTATTTGATATCTACAGACAGAAATCCACCGCCCAAAAAAATTGGAC 439
DB 101 ValgluasmilleleasppiletyrlysglungrlnserThrArsproglnlylseserasp 120
OY 440 CAGCCCATGTGTGAAGACATGAAGAGAGACGACATCTATTTGTCTGAACCTGTGA 499
DB 121 GlmprobecCyglungrlnhsglungrlnhsglungrlnhsglungrlnhsglungrln 140
OY 500 GTGCCCACCTTCTCTGTGCAAGGTTTTTGGCGCCCATTAAGACCTGCCAGGTGGCTCC 559
DB 141 ValProthrCysserleuCyelyvalphegllyahlsylyasppCyglunvalAlapro 160
OY 560 CTGACTCATGTGTTCCAGAGGCAAGAGTCAAGACTCATGATGGTATGCTGACTGTTG 619
DB 161 Leuthrhlsvalpheglnarhsglungrlnserglungrlnseraspglylealileleuval 180
OY 620 GAAAGCAAGATAGAGTCCAGGGTGTGATCAGCCGCTGAGAGACCTGTAAACTT 679
DB 181 GlyserasmaspahrgvalGlngrlyvalillesergrlnleuglnaspThrcylserThrile 200
OY 680 GAGAGTCTCAGAAAACAGAAAACAGACCTGTGTGAAATTTGATCACTTAACGCG 739
DB 201 GlungrlucysyarsgllysglungrlnleuglnleuencysglungrlnpneaspTytleuTycl 220
OY 740 ATCTGAGAGAGAGAGAACTGAAATGACCCAGCCATCACTCGAACACAGAGAGAA 799
DB 221 lleuuglungrlyarsnglungrlnmetThrglnvalilernrArgrThrglngrlnlyls 240
OY 800 CTGGAACATGTCCGAACCTTATCAGAAAGTATTCGAGTACCCTGGAAGAGTATCCAG 859
DB 241 leuuglnhsvaArghAlaleuileuileysrlyserasphsleuglnasvlaserlys 260
OY 860 TTGTGAGATGAGAGATCCAGTTCATGATGATGAGCCGCAATGCGAGTATTTCTGAGAT 919
DB 261 leuvalglunserglyileglnpnehetaspgrlnpoglnmetAlavalpheleuglnasn 280
OY 920 GCCAAGACCTGTGCAAAAAGATCGTGAAGCATCAAAAGCGTTTCAGATGAGAACTA 979
DB 281 AlalysrThrleuileuileysileserglunlaserlysalapheglnmetglulysile 300
OY 980 GAAACAAGTTATGATCATGAGCAACTCACTGTCATCTCAATAGAGAGAAAAATT 1039
DB 301 Glunhsglyrgrlyuasmecasmhlsphethrvalaenleuaspahrglungrlyle 320
OY 1040 ATCCGTGAATTTGACTTTTCTAGA-----GAAAGAGAGAGAGAGAGATGAGAGAA 1093
DB 321 lleArgrlunleasppheTyArhgrlunspgrlnuaspgrlngrlngrlngrlngrln 340
OY 1094 ATGATGAAGAGAGAGAGAGAG-----GATGCAATGAGAAATGAGAGGACGAA 1144

DB 341 Glyglungrlngrlngrlngrlngrlngrlngrlngrlngrlngrlngrlngrlngrln 360
OY 1145 AATGTCAAATPAGCATCTTCAGGGGAGAGAGAGTGTGAGAGAAAGCTGAGAGCCCTCT 1204
DB 361 AsnvalGlnthrgrlnpneProglyglunaspgrlnuaspgrlnuaspgrlnuaspgrlnu 380
OY 1205 CAGCTTCCGCAAGCTTCAGGTGCGCCCGAGAGCCACTACCTGCTCTCTCCAGAAACG 1264
DB 381 Glnval-----GlnleuglnalalalaprogllyAlaleuProvalSerseerProglunPro 398
OY 1265 TTTTGCATTCAGCAGCTGCTGCGAGATGTCCTGTGACAGAGGGAGAGTGTGCCATT 1324
DB 399 ProProAlaleuProProAlalalaspAlaprovalThr----- 411
OY 1325 GGCTCTCAGAGACACACAGTCTGAACCTTCAGGCGCTTCAGAGCGGAAACTGCGGAT 1384
DB 411 ----- 411
OY 1385 CCTTGTTTTACCCTAGTGTATTAAGGCCAAAGCCGAAACACAGCTCCAAACCACT 1444
DB 411 ----- 411
OY 1445 TGCACTATGGAGTGAAGGTCTGGGTCAATATAGCGCTCTGGGCAATTGAGATTCCAGT 1504
DB 411 ----- 411
OY 1505 GTGCAGTCCGAGAAGTGCGAGAAAGCCGCAACCAATGAGAGAGCAGAGTGAAGTAA 1564
DB 411 ----- 411
OY 1565 GAGTGTATTCAACTGCAGCTACTCTCAGATTGATTTGAGGCCCTTCTCCCAAGGA 1624
DB 412 -----GlnlleglYpheglunlApropoleuglngrly 422
OY 1625 CAGTCTCAGACCTTTGGGAGTGGGGGTGGGT-GATCTTGAAGCAGTCCCAAGTCTTC 1663
DB 423 GlnlalaAlalaproAlalaserglyserglyAlalaspserglunproAlalArghsilephe 442
OY 1684 TCCTTCTCGTGTGAATCCCTTAATGAA 1714
DB 443 SerpheserThp-Leuasmserleuasmgrln 452

RESULT 6
US-10-473-574-8
; Sequence 8, Application US/10473574
; Publication No. US20040116670A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; HAPALIA, April J.A.;
; APPLICANT: TANG, Y. Tom; YUE, Henry;
; APPLICANT: KHAN, Farrah A.; ISON, Craig H.;
; APPLICANT: BAUGHN, Mariah R.; WARREN, Bridget A.;
; APPLICANT: DUGGAN, Brendan M.; THANGAVELU, Kavitha;
; APPLICANT: HONCHELL, Cynthia D.; AZIMZAI, Valda;
; APPLICANT: ELIOTT, Vicki S.; BURROD, Neil;
; APPLICANT: DING, Li; YUE, Huidun;
; APPLICANT: BECHHA, Shanya; EMERLING, Brooke M.;
; APPLICANT: RICHARDSON, Thomas W.; LEE, Soo Yeun;
; APPLICANT: BANDMAN, Olga; LAL, Preeti G.;
; APPLICANT: LEE, Sally; GIETZEN, Kimberly J.;
; APPLICANT: CHAMLA, Narinder K.; GRIFFIN, Jennifer A.;
; APPLICANT: LEE, Ernestine A.; SWARNAKAR, Anita;
; APPLICANT: RING, Huijun Z.; JONES, Karen Anne
; TITLE OF INVENTION: CYTOSKELETON-ASSOCIATED PROTEINS
; FILE REFERENCE: PR-0918 USN
; CURRENT APPLICATION NUMBER: US/10/473,574
; PRIOR APPLICATION NUMBER: PCT/US02/09288
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 60/294,451
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/291,870
; PRIOR FILING DATE: 2001-05-18


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; PRIOR APPLICATION NUMBER: US 60/290,518
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 60/288,609
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/283,769
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/281,323
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/280,508
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO: 8
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 284191CD1
US-10-473-574-8

Alignment Scores:
Pred. No.: 5,1e-141 Length: 452
Score: 1922.50 Matches: 392
Percent Similarity: 75.14% Conservative: 22
Best Local Similarity: 71.14% Mismatches: 33
Query Match: 41.69% Indels: 105
DB: Gaps: 4

US-10-775-627a-3 (1-2590) x US-10-473-574-8 (1-452)

QY 80 ATGAGCACTTCTCGAATTACAACTTTTCTCCAAAGAGCGACGACCATGATTAAGTTC 139
DB 1 MetSer1aSerLeuAsnYrLysSerPheSerLysGluGlnGlnTrrMetAspAsnLeu 20

QY 140 GAAAGCAACGATCTGTGCTCCATCTGCTTAGAGATGTTCAAGAACCTGTGCTATTCTC 199
DB 21 GluLysGlnLeuLecYsProLecYsLeuGlnMetPheThrLysProValIleLeu 40

QY 200 CTTTGCAGCAACAACTGTGAGGAAATGTGCCAGTGCATCTTCCAGGCTCTTAACCG 259
DB 41 ProCysGlnHisAsnLeuCyArGlyCysAlaSerAspIlePheGlnAlaSerAsnPro 60

QY 260 TACTTATCCCAAGAGAGAGGAGCAACCGTGCATCAGGGGGCCCTTCCGTCTCC 319
DB 61 TyrLeuProThrArGlyGlyThrThMetAlaSerGlyArGpPheArGyCysProSer 80

QY 320 TGCAGATGAGGTGTGTTAGACAGCATGGGGTCTATGGACTGACAGAGAACTGCTC 379
DB 81 CysArGhiSgluValIleValLeuAspArGhiSgluValIleGlyLeuGlnArGAsnLeu 100

QY 380 GTGGAATAATTATTTATCTTACAGCAGGAATCCACAGGCCAGAAAAAAATTSAG 439
DB 101 ValGluAsnIleIleAspIleTyrLysGlnIleSerThrArGProGluLysSerAsp 120

QY 440 CAGGCCATGTGTGAAGAGCATGAAGAGAAAGCATCAACATCTTGTCTGAATTGGA 499
DB 121 GlnProMetCysGluGlnHisGluGlnIleAsnIleTyrCysLeuAsnCySglu 140

QY 500 GTGCCCACTGTCTCTTGTGCAAGTTTGGCCCAATAGAGCTGCGAGGAGGCTCCC 559
DB 141 ValProMetCysSerLeuCySlyValAlaPheGlnValAlaHisAspCySgluValAlaPro 160

QY 560 CTGACTCATGTGTTCCAGAGGAGCAAGTCAAGCTCAGTGTGATTTGCTGTAAGTGTG 619
DB 161 LeuThrHisValAlaPheGlnArGlnLysSerGluLeuSerArGpIleAlaIleLeuVal 180

QY 620 GGAAGCAACGATAGAGTCCAGGGGTGTATCAGCCAGCTGAGGAGCACTGTGAAAACAT 679
DB 181 GlySerAsnAspArGValGlnGlyValIleSerGlnLeuGlnAspThrCySlyArThrIle 200

QY 680 GAGAGTGTCTGCAAGAAAGCAAGAACTGTGTGAGAAATTTGATCACTTATAGGC 739
DB 181 GAGAGTGTCTGCAAGAAAGCAAGAACTGTGTGAGAAATTTGATCACTTATAGGC 739
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DB 201 GluGluCysArGlySgluLysGlnIleLeuCySgluLysPheAspTyrLeuTyrGly 220
QY 740 ATCTTGAGAGAGGAGAACTGAAATGACCAAGCCATCTCTGAAACAGAGAGAA 799
DB 221 IleLeuGlnIleArGlySAsnGlnMetTrGlnValIleThrArGTrGlnGlnLys 240
QY 800 CTGGAACATGTCGAATCTTATCAGAGATTTCCGATCACTCGAGAGAACTATCCAG 859
DB 241 LeuGlnHisValArGAlaLeuLysLysTyrSerAspHisLeuGlnAsnValSerLys 260
QY 860 TTGAGAGTCAAGAAATCCAGTTCAATGATAGACCCGAAATGGCAATTTCTGCAAT 919
DB 261 LeuValGlnSerGlyIleGlnPheMetAspGluProGluMetAlaValPheLeuGlnAsn 280
QY 920 GCCAAGACCTGTGCAAAAGATCTGGAAGCATCAAGGCTTTTCAATGAGAAACTA 979
DB 281 AlaLysThrLeuLeuLysLysIleSerGlnAlaSerLysAlaPheGlnMetGluLysIle 300
QY 980 GAAACAGTTATGAGATCAATGAGCAACTTCACTGTCATCTCAATGAGAGAAAAATT 1039
DB 301 GluHisGlyTyrGluAsnMetCAsnHisPheThrValAsnLeuAsnArGlnGluLysIle 320
QY 1040 ATCCGTGAATTAATGACTTTTCTAGA-----GAAAGAGAGAGAGAGATGAGAGAA 1093
DB 321 IleArGlnIleAspPheTyrArGlnAspGluAspGlnGlnIleGlnGlnLys 340
QY 1094 ATGATGAGAGAGAGAGAGAGAG-----GATGCACTAAGATGAGAGAGAGAA 1144
DB 341 GlyLysGlnGlnIleGlnGlnGlnValAlaGlyGlnAlaValAlaGlnGlnValGln 360
QY 1145 AATGTTCAATATACATCTTCAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1204
DB 361 AsnValGlnThrGluPheProGlyGlnAspGluAsnProGluLysAlaSerGlnLeuSer 380
QY 1205 CAGCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1264
DB 381 GlnVal-----GluLeuGlnAlaIleAlaProGlyAlaLeuProValSerSerProGluPro 398
QY 1265 TTTTCATCCATGCGAAGCTGCTGTCAGATGTCCTGCTGTCACAGAGAGAGAGAGAG 1324
DB 399 ProProAlaLeuProProAlaAlaAspAlaProValThr----- 411
QY 1325 GGCTTCAGAGAGACACAGCTGTAACCTTGAGGCCCTTCAGAGAGAGAGAGAGAG 1384
DB 411 ----- 411
QY 1385 CCCTGTTTAACTTATGTTGATTAAGGCCAAAGCCGAAAGACAGCTCCAAACCACT 1444
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QY 1445 TGCATCTCAGGAGTGAAGGTCTGGGTCAATAGGCCCTCTGGGCAATTGAGATTCCAGT 1504
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QY 1505 GTGCAGTCCGAGAGAGTGGAGAGAGCCGCAACCAATGAGCAGCAGCAGTGTGAAG 1564
DB 411 ----- 411
QY 1565 GAGTCTAGTTCAATGCACTGACGCTACTCTCAGATTGATTTGAGGCCCTTCTCCCAAGGA 1624
DB 412 -----GlnIleGlyPheGlnAlaProProLeuGlnGly 422
QY 1625 CAGTCTGACAGCTTGGGAGAGTGGGGGTGGGGT-GATCTGAGCAGCAGCTGCGACGTTCT 1683
DB 423 GlnAlaAlaIleProAlaSerGlySerGlyAlaAspSerGluProAlaArGHisIlePhe 442
QY 1684 TCCCTTCCTCGGTTTGAATTCCTTAATGAA 1714
DB 443 SerPheSerTrp-LeuAsnSerLeuAsnGln 452

RESULT 7
US-09-764-864-821
; Sequence 821, Application US/09764864
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; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIORITY FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 821
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-764-864-821

Alignment Scores:
Pred. No.: 1,96e-126 Length: 414
Score: 1735.50 Matches: 355
Percent Similarity: 73.29% Conservative: 21
Best Local Similarity: 69.20% Mismatches: 33
Query Match: 37.64% Indels: 105
DB: 9 Gaps: 4

US-10-775-627a-3 (1-2590) x US-09-764-864-821 (1-414)

QY 194 ATCTCCCTTGCGACACACCTGTGACGAAATGTGCCAGTACATCTTCAGGCTCT 253
DB 1 IleuProCySgInHieAsnLeuCySArGlyScSaIaSerAapIlePheGlnAlaSer 20
QY 254 AACCCGTACTTAACCAAGAGAGGCGACACCGTGGCATCAGGGGGCCGCTCCGCTGT 313
DB 21 AsnProTyrLeuProThArGlyGlyThrThrMetAlaSerGlyGlyArGpHeArGys 40
QY 314 CCCTCCCTGACAGATGAGTGGTGTAGACAGACATGGGGTCTATGACTCAGCAGAGAAC 373
DB 41 ProSerCySArGhSgInVaIValLeuAspArGhSgIlyValTyrGlyLeuGlnArGAsn 60
QY 374 CTGCTCGTGAAGAAATATTGATATCTTAACAGACAGAAATCCACAGGCGCAGAAAAA 433
DB 61 LeuLeuValGlnAAsnIleIleAspIleTyrIlySgInGlnuSerThArGProGlnuSlys 80
QY 434 TTGACACGACCATGTGTGAAGAGCATGAAGAGAACCATCAATCTATTGTCTGAAC 493
DB 81 SerAspGlnProMeCySgInGlnuHieSgInGlnuArGlyIleAsnIleTyrCysLeuAsn 100
QY 494 TGTGAAGTGGCCCACTGTTCTGTGCAAGGTTTGTGGCGCCCATPAAGACCTGCCAGGTG 553
DB 101 CysGlnuAlProThnCysSerLeuCySgIlyValPheGlyAlaHieSlyAspCysGlnuAl 120
QY 554 GCTCCCTGACTCATGTGTTCCAGAGGACAGAGTCAAGCTCAGTATGATGTTGCTGTA 613
DB 121 AlaProLeuThrHieValPheGlnArGInlySerGlnuLeuSerAapGlyIleAlaIle 140
QY 614 CTGTGGGAAGCAGATAGAGTCCAGGGTGTGATCAGCCAGCTGGAGACACCTGTAA 673
DB 141 LeuValGlySerAsnAspArGlyValGlnIlyValIleSerGlnLeuGlnAspThrCysSlys 160
QY 674 ACTATTGAGAGTGTGTCAGAGAAAGCAAGAACGACCTGTGTGGAATTTGATGACCTA 733
DB 161 ThrIleGlnuGlnuCySArGlySgInlySgInGlnuSlysGlnuLysPheAspTyrLeu 180
QY 734 TAAGCATCTGAGAGAGAGAGACGTAAATGACCCAAAGCCATCATCTGAAACAGAG 793
DB 181 TyrGlyIleLeuSgInGlnuArGlySgInGlnuMetThrGlnuValIleThrArGThrGlnu 200
QY 794 GAGAACTGGAACATGTCCGAATTTATCAGAAAGTATTCGATCAGCTGAGAACTGA 853
DB 201 GlnuSlysLeuGlnuHieValArGAlaLeuIleuSlyTyrSerAspHieLeuGlnuSval 220
QY 854 TCCAGTGTGTGAGTCAAGAAATCCAGTTCATGATGAGTCCCGGAAATGGCAGTATTTCTG 913
DB 221 SerlyLeuValGlnuSerGlyIleGlnPheMetAspGlnuProGlnuMetAlaValPheLeu 240
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QY 914 CAGAAATCCAAAGCCCTGTGGCAAAAGATCGTGAAACATCAAAAGCGTTTCAGATGAG 973
DB 241 GlnAsnAlaYsThrLeuLeuSlyIleSerGlnuAlaSerIlySAlaPheGlnMetGln 260
QY 974 AAATGACAAAGGTTATGATCATAGACAACTTCACTGCAATCTCAATAGAAAGAA 1033
DB 261 LysIleGlnuSgIlyTyrGlnuAsnMetAsnHiePheThrValAsnLeuAsnArGlyGlnu 280
QY 1034 AAATTAATCCGTAATTAATGACTTTTCTAGA-----GAAGAGGAAGGAAGAATGCA 1087
DB 281 LysIleIleArGlnuIleAspPheTyrArGlnuAspGlnuSgInuSgInuGlnuGly 300
QY 1088 GAGAAATAGATGAAGAGAGAGAGAGAG-----GATCAGATGAAATGAGAG 1138
DB 301 GlyGlnuGlyGlnuArGlnuGlyGlnuGlyGlnuValGlyGlyGlnuAlaValGlnuGlnu 320
QY 1139 GCAGAAATATGTTCAAAATAGCATCTTCAGGGGAAAGAGAGAGTGGAGAAAGTGCAGAG 1198
DB 321 ValGlnuSvalGlnuThrGlnuPheProGlyGlnuAspGlnuSgInuSgIlySAlaSerGlnu 340
QY 1199 CCCTCAGGCTCCCGCAGAGCTTCAGAGTGCAGCCCGCAGAGCCACTACCTGCTCCTCCA 1258
DB 341 LeuSerGlnuVal-----GlnuGlnuAlaIleProGlyAlaLeuProValSerSerPro 358
QY 1259 GAACCGTTTTCATCATGACCACTGCTGACAGATGCTCTGTGACACAGGGGAGGTGTG 1318
DB 359 GlnuProProAlaLeuProProAlaLeuProAlaAlaSerAlaProValThr----- 373
QY 1319 CCATTTGGCTCTCAGCAGACCAACAGCTGTGAATCTCAGGCCCTTCAGAGCGGAACCT 1378
DB 373 ----- 373
QY 1379 GCGGATCCCTGTTTACCTAGTTGGTATAAAGGCCGGAAGAACAGTCCAAC 1438
DB 373 ----- 373
QY 1439 CAACCTTGACATCAGAGAGTGAAGGTCTGGTCAATAGAGGCTTGAGCATTTAGAGAT 1498
DB 373 ----- 373
QY 1499 TCCAGTGTGACGTCCGAGAGAGTGGCAGAGCCGCAACCAATGACAGCAGATGAGT 1558
DB 373 ----- 373
QY 1559 GGTAAAGATCTAGTTCACTGACGAGTACCTTCAGATGAGATTGAGGCCCTTCTCCC 1618
DB 374 -----GlnIleGlyPheGlnuAlaProProLeu 382
QY 1619 CAGGACAGTCTGACAGCTTGGGAGAGTGGGGGTGGGT--GATCCTGAGCCAGCTCGCCAC 1677
DB 383 GlnuIlyGlnuAlaAlaIleProAlaSerGlySerGlyAlaAspSerGlnuProAlaArGhS 402
QY 1678 GTCTTCTCTTCTCTCTGTTGAATTCCTTAATGAA 1714
DB 403 IlePheSerPheSerTyrLeuAsnSerLeuAsnGlnu 414

RESULT 8
US-09-890-688-58
; Sequence 58, Application US/09890688
; Publication No. US20030144475A1
; GENERAL INFORMATION:
; APPLICANT: Seishi KATO
; APPLICANT: Chikashi EGUCHI
; APPLICANT: Mihoro SAKI
; TITLE OF INVENTION: Human Proteins and cDNAs thereof
; FILE REFERENCE: 2001-1102A/MMC/00653
; CURRENT APPLICATION NUMBER: US/09/890,688
; PRIORITY FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: JP 11-346863
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: JP 11-34684
; PRIOR FILING DATE: 1999-12-06
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; PRIOR APPLICATION NUMBER: JP 2000-31062
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: JP 2000-34091
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: JP 2000-34090
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: JP 2000-35829
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: JP 2000-35899
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: JP 2000-71161
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: JP 2000-160851
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 58
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-890-688-58

Alignment Scores:
Pred. No.: 5,29e-82 Length: 358
Score: 1166.00 Matches: 228
Percent Similarity: 77.62% Conservative: 46
Best Local Similarity: 64.59% Mismatches: 73
Query Match: 25.29% Indels: 6
Gaps: 3

US-10-775-627a-3 (1-2590) x US-09-890-688-58 (1-358)

QY 80 ATGAGCACTTCTGTAATTAACAAGTCTTTCTCCAAAGACGACGACCATGATACTTG 139
DB 1 MetasphertherValIglYpneUleuGlYasPalaHisSerMetAspAnleu 20

QY 140 GAAAGCACTGATCGTCCATCGCTAGATGTTTCAAGAGCCGTGGTCACTTC 199
DB 21 GluYsgInleuIleCysProIleCysleuGlUmetPheSerIlyProValIleu 40

QY 200 CCTTGACGACCAACCTGTGAGGAAATGTGCCAGTCACTTCCAGGCTCTTAACCCG 259
DB 41 ProCysGlnHisAnleuCyBaIrgLycSaIaAnspValPheGlnAlaSerAnPro 60

QY 260 TACTTACCCACAGAGAGGACCAACCGTGCATCAAGGCGCGCTTCCGCTGCCCTCC 319
DB 61 LeuTrpGlnSerArgIlySerThrValSerSerGlyIArgPheArgCysProSer 80

QY 320 TGCAGACATGAGTGTGTTAAGACACATGGGGTCTATGACTGACAGAGAACTGCTC 379
DB 81 CysArgHisGluValValLeuAspArgHisGluValIlyrGlyLeuGlnArgAnleu 100

QY 380 GTGAAAAAATTTATTTGATATCTTAACAAGAGATCCACAGGCCA---GAAAAAAATTG 436
DB 101 ValGlnAnleuIleIleAspIleIlyrLysGlnIlySerSerArgProLeuHisSerIlyAla 120

QY 437 GACCAAGCCC---ATGTGTGAAGACATGAAGAGGACGACATCAATCTATTGTGTAAC 493
DB 121 GlnIlyHisLeuMetCysGlnGlnIlyHisGlnIlyGlnIlySerIleAnleuIlyrCysLeuSer 140

QY 494 TGTGAATGCCACCTGTTCTTGTGCAAGGTTTGGCGGCCATAAGACTGCAAGTG 553
DB 141 CysGlnValProThrCysSerLeuCysIlyValPheGlyAlaHisIlyAspCysGlnVal 160

QY 554 GCTCCCTGACTCATGTGTTTCCAGAGGACGAAGTCAAGGCTCATGATGATGCTGTA 613
DB 161 AlaProLeuProThrIleIlyrLysArgIlyHisSerGlnIlySerArgPylIleAlaMet 180

QY 614 CTGTGGAGCAACGATAGAGTCCAGGGTGTGTCAGCCAGCTGAGAGACACTGTAA 673
DB 181 LeuValIlaGlyAsnAspArgValIglAlaValIleThrGlnMetGlnIlyValCysGln 200

QY 674 ACTATTGAGAGTGCTGTGAGAAAGAGAAACAGGACCTGTGTGAAATTGATCACTTA 733

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DB 201 ThrIleGluAspAnSerArgIlyrGlnIlySerIleuAnIlyrPheGlnIlySerLeu 220
QY 734 TACGCATCTCTGGAGAGAGAGAACTGAATATACCCAGCCCTCATCTGAACACAGAG 793
DB 221 CysAlaValLeuIlyGlnIlyrGlySerGlyGlnIlySerIleuGlnAlaLeuAlaIrgGlnIly 240
QY 794 GAGAACTGGAACATGCTCGGAACCTTATCAGAGATATTCGATCAGCCGTGAGAACGTA 853
DB 241 GlnIlyLeuGlnArgValArgGlyLeuIleArgGlnIlyrGlyAspHisLeuGlnAlaSer 260
QY 854 TCCAGTGTGTGAGTCAAGAAATCCAGTTCATGATGATGAGCCGCAATGCGATATTCTG 913
DB 261 SerIlyLeuValGlnSerAlaIleGlnSerMetGlnIlyProGlnMetAlaLeuIlyrLeu 280
QY 914 CAGATGCCAAGACCTGTGTCAAAGATCGTGAAGCATCAAGGCCGTTTCAGATGAG 973
DB 281 GlnGlnAlaIlySerIleuIleAnleuIlyValIglAlaMetSerIlyValIglIleuAlaGly 300
QY 974 AAACTAGAACAGGTTATGATCATGACCAACTTCACTGTCAATGCAATGAGAA 1033
DB 301 ArgProGlnProGlyIlyrGlnSerMetGlnIlyPheThrValArgValIgluHisValAla 320
QY 1034 AAATATTACCGTGAATTGACTTT-----TCTAAGAGAGAGAGAGAGAA 1081
DB 321 GluMetLeuArgThrIleAspPheGlnProGlyAlaSerGlyGlnIlyGlnIlyValAla 340
QY 1082 GATGCAGAGAAATATGATGAAGAGAGAGAGAGAT 1120
DB 341 ProAspGlyGlnIlySerAlaGlyProGlnIlyGln 353

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RESULT 9

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US-09-908-988B-2
; Sequence 2, Application US/09908988B
; Patent No. US20020127690A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; FILE REFERENCE: MYOG:028US
; CURRENT APPLICATION NUMBER: US/09/908,988B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-908-988B-2

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Alignment Scores:

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Pred. No.: 1,09e-81 Length: 366
Score: 1162.00 Matches: 226
Percent Similarity: 76.99% Conservative: 55
Best Local Similarity: 61.92% Mismatches: 76
Query Match: 25.20% Indels: 8
Gaps: 4

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US-10-775-627a-3 (1-2590) x US-09-908-988B-2 (1-366)

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QY 80 ATGAGCACTTCTGTAATTAACAAGTCTTTCTCCAAAGACGACGACCATGATACTTG 139
DB 1 MetAspPheThrValIglYpneUleuGlYasPalaHisSerMetAspAnleu 20

QY 140 GAAAGCACTGATCTGTCCATCTGCTTAAGATATTTCAAGAGCCGTGGTCACTTC 199
DB 21 GluYsgInleuIleCysProIleCysleuGlUmetPheSerIlyProValIleu 40

QY 200 CCTTGACGACCAACCTGTGAGGAAATGTGCCAGTCACTTCCAGGCTCTTAACCCG 259

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OY	260	TACTTACCACAAAGAGAGAGACACACCTGGTCATCAGGGGGCCGCTTCCTGCTCCCTCC	319
Db	61	LeutPrgInSerArgLYSerThrThrValaSerSerGlyLYAlaRgPheArgCYsProSer	80
OY	320	TGCAGACATGAGGTGTGTAGACAGACATGGGGGTCTTAGACCTGACAGGAAACCTGCCTC	379
Db	81	CysAlaGh1sGLValValLeuAspArgH1sGLValLYrGLYLeuGlnArgAsnLeuLeu	100
OY	380	GTGGAAAACATTATTTGATATCTACAAAGCAAGAACTCCACAGGCCA---GAAAAAATTG	436
Db	101	ValGluAsn1le1leAsp1leTYrLYrLYsGlnGlnSerArgProLeuH1sAlaLYsAla	120
OY	437	GACCAAGCCC---ATGTGTCAAGACATGAAAGAGAAAGCATCAACTCTATTGTCTGAAC	493
Db	121	GINGlnH1sLeuMetCYsGLGlnH1sGLAspGlnLY1leAsn1leTYrCYsLeuSer	140
OY	494	TGTGAAGAGCCCACTGGTCTCTTGCAAGAGTTTGGGCGCCATPAAGACCTCCAGAG	553
Db	141	CysGLValAlProTHnCysSerLeuCYsLYsValPheGLYAlaH1sLYsAspCYsGLVal	160
OY	554	GCTCCCTGCATCATGTGTCTTCAGAGCCAGAACTCAGAGCTCATGTAGTATTGCTGTGA	613
Db	161	AlaProLeuProTHr1leTYrLYsArgGlnLYsSerGlnLeuSerAspGLY1leAlaMet	180
OY	614	CTTGCGGAGACAAAGATPAGATCCAGGGGTGTGATCAGCCAGCTGGAGACACCTGTAA	673
Db	181	LeuValAlaGLYAsnAspArgValGlnAlaVal1leTHrGlnMetGlnGlnValCYsGln	200
OY	674	ACTATTGAGAGAGTGTGCGAAGAGAGAAACAGAACCTGTGTGAGAAATTGATCCCTGA	733
Db	201	Thr1leGLYAspAsnSerArgArgGlnLYsGlnLeuAsnGlnArgHegGlnThrLeu	220
OY	734	TACGGCATCTTGAGAGAGAGAGAACTGAAATGACCACCAAGCATCACTGAAACAGAG	793
Db	221	CysAlaValLeuGlnGlnLYsArgLYsGlnLeuLeuGlnAlaLeuAlaArgGlnGlnGln	240
OY	794	GAGAAACCTGGAAACATGTCGCACTCTTATCAGAGAAATATCCGATACCTGGAGAAAGTA	853
Db	241	GlnLYsLeuGlnArgValArgLYsLeu1leArgGlnTYrGLYAspH1sLeuGlnGlnSer	260
OY	854	TCCAAAGTTGAGAGTGCAGAACTCAGTTCATGAGATGAGACCCGAAATGGCAGATTTCTG	913
Db	261	SerLYsLeuValGlnSerAla1leGlnInSerMetGlnGlnProGlnMetAlaLeuTYrLeu	280
OY	914	CAGAAATGCCAAGACCTGTTCGAAAAGATCGTGAAGATCAAAAGCGCTTTCAGATGGAG	973
Db	281	GlnGlnAlaLYsGlnLeu1leAsnLYsValGlnAlaMetSerLYsValGlnLeuAlaGLY	300
OY	974	AAACTGAGAACAGGTTATGAGATCATGAGACACTTCATCTGTCAATCTCAATGACAGAA	1033
Db	301	ArgProGlnProGlnTYrGlnSerMetGlnGlnPheSerValSerValGlnH1sValAla	320
OY	1034	AAAATTATCCGGAATTGACTTT-----TTCAGAGAAAGAGAAAGAGAGAAAGAT	1088
Db	321	GlnMetLeuArgThr1leAspHegGlnProGlnLYsAlaGLYAspGlnAspAspAsp	340
OY	1085	GCAGAGAAATAGATGAAGAGAGAGAGAA-----GAGCATGCAGTGAAGATGA	1133
Db	341	MetAlaLeuAspGLYGlnGlnGlnAsnAlaGLYLeuGlnGlnGlnLYsGlnAspValPro	360
OY	1136	GAGGCGAGAAATGTT 1150	
Db	361	GlnGlnSerGlnLYs 365	

RESULT 10
US-10-775-649-2
; Sequence 2, Application US/10775649
; Publication No. US20040132160A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.

	TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROVIBRILES FILE REFERENCE: MYOG:028USD2 CURRENT FILING DATE: 2004-02-10 PRIOR APPLICATION NUMBER: 09/908,988 PRIOR FILING DATE: 2001-07-18 PRIOR APPLICATION NUMBER: 60/219,020 PRIOR FILING DATE: 2000-07-18 NUMBER OF SEQ ID NOS: 6 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2 LENGTH: 366 TYPE: PRF ORGANISM: Mus musculus US-10-775-649-2			
	Alignment Scores: Pred. No.: 1,09e-81 Length: 366 Score: 1162.00 Matches: 226 Percent Similarity: 76.99% Conservative: 55 Best Local Similarity: 61.92% Mismatches: 76 Query Match: 25.20% Indels: 8 Ds: 16 Gaps: 4			
QY	US-10-775-627A-3 (1-2590) x US-10-775-649-2 (1-366)			
QY	80 ATGACACACTCTCTGCAATTACAAAGCTTTCACAAAGACAGACAGACCATGATTAATTCTG	139		
Db	1 MetanpheithValGlyPheIysProIeuIeuGlyAspAlaHisAsnMetAspAsnLeu	20		
QY	140 GAAAAGCAACTGATCTGTCCACTTCGCTTAGAGATGTTACAGAAAGCTGTGGTCAATTCTC	199		
Db	21 GlyIysGlnLeuIleCysProIleCysLeuGlnMetPheSerIysProValIleLeu	40		
QY	200 CCTTGCCACGACAACTCTGCGACGAAATGTGCACAGATCACTTCCTCAGGCTTACACCG	259		
Db	41 ProCysGlnHisAsnLeuCysArgIysCysAlaAsnAspValPheGlnIaSerAsnPro	60		
QY	260 TACTTACCACAAAGAGAGGACCAACCGTGATGACGAGGAGCGCTTCGCTGTCCCTCC	319		
Db	61 LeuTrpGlnSerIaArgGlySerThrThrValSerSerGlyIaArgPheArgCysProSer	80		
QY	320 TGCACACATGAGGTGGTGTTAACACACATGGGGGTCTATGACTGCAAGAACTGTCTC	379		
Db	81 CysArgHisGlnValValLeuAspArgHisGlyValIaIaGlyLeuGlnIaArgAsnLeu	100		
QY	380 GTGGAAACATTAATTGATTCATCACAGACGAATATCACACAGGCA--GAAAAAAATTG	436		
Db	101 ValGlnAsnIleIleAspIleIaIysGlnGlnIaSerArgProIeuHisAlaIaIysAla	120		
QY	437 GACCAAGCCC--ATGTGTAAAGAGCATGAAGAAAGCATCAACATCTATTGTCTGAAC	493		
Db	121 GlnGlnHisIaIeuMetCysGlnGlnIaIleGlnIaGlnValIleAsnIleIaIysCysLeuSer	140		
QY	494 TGTGAAGTCCCAACCGTTCCTCTTGCGACAGGTTTTTGCGCCCATTAAGACCTGCAGTGS	553		
Db	141 CysGlnValProIaIaCysSerIeuCysIysValIaPheGlyAlaHisIaIysAspCysGlnVal	160		
QY	554 GCTCCCTGACTCATGTATTTCCAGAGGCGCAGAGTCAAGCTCAAGTCAATGATGATAGCTGTA	613		
Db	161 AlaProIeuProThrIleIaIaIysArgGlnIaIysSerGlnIaIeuSerAspGlyIleAlaMet	180		
QY	614 CTGTGGGAAAGCAAGATPAGATCCAGGGGTGTGATCAGCCAGCTGGAGACACTGTAA	673		
Db	181 LeuValIaIaGlyAsnAspArgValGlnIaIaValIleIleThrGlnMetClnGlnIaCysGln	200		
QY	674 ACTATTGAGAGAGTGCCTGCAGAAAGACGAAACAGGACCTGTGTGAGAAATTGTATGACCTTA	733		
Db	201 ThrIleGlnAspAsnSerArgArgGlnIaGlnIaIeuLeuAsnGlnIaArgPheGlnThrLeu	220		
QY	734 TACGGCATCTCTGAGAGAGAAAGCATGAATGACCCAAAGCATCACTGAAACACAGAG	793		

Db 221 CysAlaValLeuGluGluArgLysGlyGluLeuLeuGlnAlaLeuAlaArgGluGlnGlu 240
 Qy 794 GAGAAACCTGGAACATGTCGGAACCTTTATCGAAGATTTCCGATTCACCTTGGAAGCTA 853
 Db 241 GluLysLeuGlnAlaArgValArgGlyLeuAlaLeuGlnTyrgLysAspHisLeuGluGlySer 260
 Qy 854 TCCAAAGTGTGGAGTCAGCAATCCAGTTCATGATGATGAGCCGAAATGGCAGTATTCTG 913
 Db 261 SerLysLeuValGluSerAlaIleGlnSerMetGluGluProGlnMetAlaLeuTyrlleu 280
 Qy 914 CAGAAATGCCAAGACCTGTGCAAAAGATCGTGAAGCATCAAGCGCTTTCAGATGAG 973
 Db 281 GlnGlnAlaLysGluLeuAlaAsnLysValGlyAlaMetSerLysValGluLeuAlaGly 300
 Qy 974 AAATAGCAACAAGTTATGATGATATGAGCAATTCATCTCATCTTCATATAGAGAA 1033
 Db 301 ArgProGluProGlyTyrgLysSerMetGluGlnPheSerValSerValGlnHisValAla 320
 Qy 1034 AAAATTATCCGTGAATATGACTTT-----TCTAGAGAAAGAGAGAGAGAGAT 1084
 Db 321 GluMetLeuArgThrIleAspPheGlnProGlyAlaAlaGlyAspGluGluAspAsp 340
 Qy 1085 GCAGAGAAATAGATGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1135
 Db 341 MetAlaLeuAspGlyGluGluGlyAsnAlaGlyLeuGluGluGluArgLysLeuAspValPro 360
 Qy 1136 GAGCAGCAAAATGTT 1150
 Db 361 GluGlySerGlyLeu 365

RESULT 11

US-10-775-627-2
 ; Sequence 2, Application US/10775627
 ; Publication No. US2004014246A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OLSON, ERIC
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
 ; TITLE OF INVENTION: AND INTERMEDIATE FILAMENTS IN STRIATED MUSCLE CELLS
 ; FILE REFERENCE: WOG:0280SD1
 ; CURRENT APPLICATION NUMBER: US/10/775,627
 ; PRIOR FILING DATE: 2004-02-10
 ; PRIOR APPLICATION NUMBER: 09/908,988
 ; PRIOR FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: 60/219,020
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 366
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-775-627-2

Alignment Scores:

Pred. No.: 1.09e-81 Length: 366
 Score: 1162.00 Matches: 226
 Percent Similarity: 76.99% Conservatave: 55
 Best Local Similarity: 71.92% Mismatches: 76
 Query Match: 25.20% Indels: 8
 DB: 16 Gaps: 4

US-10-775-627a-3 (1-2590) x US-10-775-627-2 (1-366)

Qy 80 ATGAGCACTTCTGGAATTACAGTCTTTCTCAAGAGCAGAGACCATGATTAAGTCTG 139
 Db 1 MetAsnPheThrValGlyPheLysProLeuGluLysAspAlaHisAsnMetAspAsnLeu 20
 Qy 140 GAAAGCAACATGATGTCCTCATCTGCTTAGAGATGTTTCAGAGAGCCCTGTGTATCTC 199
 Db 21 GluLysGlnLeuIleCysProIleCysLeuGlnMetPheSerLysProValIleAlaLeu 40
 Qy 200 CTTGCAGACAACTGTGACAGAAATGTGCCAGTGCATCTTCCAGGCTTAACCG 259

Db 41 ProCysGlnHisAsnLeuCysArgLysCysAlaAsnAspValPheGlnAlaSerAsnPro 60
 Qy 260 TACTTACCCCAAGAGAGGACACACCTGTGCATCAGAGGGCCGCTTCCGCTGTCCCTCC 319
 Db 61 LeuTrpGlnSerArgGlySerThrThrValSerSerIleGlyArgPheArgCysProSer 80
 Qy 320 TGCAGACATAGAGGTGGTGTAGACAGCATGGGGGTCTATGAGACTGTCAGAGAACTCTC 379
 Db 81 CysArgHisGluValValLeuAspArgHisGlyValTyrgLysLeuGlnArgHisLeuLeu 100
 Qy 380 GTGGAATAACATTATTTGATATCTCAAGACAGAAATCCACAGAGCA--GAAAAAATTG 436
 Db 101 ValGlnAsnIleIleAspIleTyrgLysGlnLysSerLysArgProLeuHisAlaLysAla 120
 Qy 437 GACCAAGCC--ATGTGTGAAGACATGAAGAGAAAGCATCAACATCTATTGTTCGAC 493
 Db 121 GluGlnHisLeuMetCysGluGlnHisGluAspGluLysIleAsnIleTyrgCysLeuSer 140
 Qy 494 TGTGAAGTGGCCACCTGTTCTGTGCAAGCTTTTGGCGCCATAGAAGCTCCAGCTG 553
 Db 141 CysGluValProThrCysSerLeuCysLysValPheGlyAlaHisLysAspCysGluVal 160
 Qy 554 GCTCCCTGACTCATGTGTTCCAGAGGAGAGAGTCAAGAGTCAAGTCAATGATGTATGCTGTA 613
 Db 161 AlaProLeuProThrIleTyrgLysArgGlnLysSerGluLeuSerHisGlyIleAlaMet 180
 Qy 614 CTTGTGGAAAGCAAGATAGATGTCAGAGGTGTATGATCAGCCAGCTGAGAGACCTGTAA 673
 Db 181 LeuValAlaGlyAsnAspArgValGlnAlaValIleThrGlnMetGluGluValCysGln 200
 Qy 674 ACTATTGAGAGAGTGTGCAGAAAGCAAGAAACAGAGACTGTGTGAAGAAATTGATCACTTA 733
 Db 201 ThrIleGlnAspAsnSerArgArgGlnLysGlnLeuLeuAsnGlnArgPheGlnThrLeu 220
 Qy 734 TACGCACTCTGAGAGAGAGAGAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGAGAG 793
 Db 221 CysAlaValLeuGluGluArgLysGlyGluLeuLeuGlnAlaLeuAlaArgGluGlnGlu 240
 Qy 794 GAGAACTGGAACATGTCGGAACCTTTATCGAAGATTTCCGATTCACCTTGGAAGCTA 853
 Db 241 GluLysLeuGlnAlaArgValArgGlyLeuAlaArgGlnTyrgLysAspHisLeuGluGlySer 260
 Qy 854 TCCAAAGTGTGGAGTCAGCAATCCAGTTCATGATGATGAGCCGAAATGGCAGTATTCTG 913
 Db 261 SerLysLeuValGluSerAlaIleGlnSerMetGluGluProGlnMetAlaLeuTyrlleu 280
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 Db 301 ArgProGluProGlyTyrgLysSerMetGluGlnPheSerValSerValGlnHisValAla 320
 Qy 1034 AAAATTATCCGTGAATATGACTTT-----TCTAGAGAAAGAGAGAGAGAGAT 1084
 Db 321 GluMetLeuArgThrIleAspPheGlnProGlyAlaAlaGlyAspGluGluAspAsp 340
 Qy 1085 GCAGAGAAATAGATGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1135
 Db 341 MetAlaLeuAspGlyGluGluGlyAsnAlaGlyLeuGluGluGluArgLysLeuAspValPro 360
 Qy 1136 GAGCAGCAAAATGTT 1150
 Db 361 GluGlySerGlyLeu 365

RESULT 12

US-10-204-921-57
 ; Sequence 57, Application US/10204921
 ; Publication No. US20050095587A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.

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; APPLICANT: PANZER, Scott R.
; APPLICANT: SPIRO, Peter A.
; APPLICANT: BANVILLE, Steven C.
; APPLICANT: SHAH, Puri I.
; APPLICANT: CHALUP, Michael S.
; APPLICANT: CHANG, Simon C.
; APPLICANT: CHEN, Alice
; APPLICANT: D'SA, Steven A.
; APPLICANT: AMSHEY, Stefan
; APPLICANT: DAHL, Christopher R.
; APPLICANT: DAM, Tam C.
; APPLICANT: DANIELS, Susan E.
; APPLICANT: DUFOUR, Gerard E.
; APPLICANT: FLORES, Vincent
; APPLICANT: FONG, Willy T.
; APPLICANT: GREENAWALT, Lila B.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: JONES, Anissa L.
; APPLICANT: LITV, Tommy F.
; APPLICANT: ROSEBERRY, Ann M.
; APPLICANT: ROSEN, Bruce H.
; APPLICANT: RUSSO, Frank D.
; APPLICANT: STOCKREHER, Theresa K.
; APPLICANT: DAPRO, Abel
; APPLICANT: WRIGHT, Rachel J.
; APPLICANT: YAP, Pierre E.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: BRADLEY, Diana L.
; APPLICANT: BRATCHER, Shawn R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: COHEN, Howard J.
; APPLICANT: HODGSON, David M.
; APPLICANT: LINCOLN, Stephen E.
; APPLICANT: JACKSON, Stuart
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1133 PCT
; CURRENT APPLICATION NUMBER: US/10/204,921
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/185,213; 60/205,285; 60/205,232; 60/205,323; 60/205,287;
; 60/205,324; 60/205,286
; PRIOR FILING DATE: 2000-02-24; 2000-05-17; 2000-05-16; 2000-05-17; 2000-05-17;
; 2000-05-17; 2000-05-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PERL Program
; SEQ ID NO 57
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID NO: IG:247384.1,orf2:2000WAY19
US-10-204-921-57

Alignment Scores:
Pred. No.: 6.24e-80 Length: 366
Score: 1139.50 Matches: 226
Percent Similarity: 73.47% Conservative: 51
Best Local Similarity: 59.95% Mismatches: 77
Query Match: 24.71% Indels: 23
DB: 17 Gaps: 3

US-10-775-627a-3 (1-2590) x US-10-204-921-57 (1-366)
QY 83 AGCACTTCTGATTAACAAG---TCTTCTCAAGAGAGAGACAGACCATGATTAATTG 139
DB 11 SerHisArgMetAspTyrLysSerSerLeuLeuIleGlnAspGlyAsnProMetGlnuSmLeu 30
QY 140 GAAAGCAATGATGTGTCCATCTGCTAGAGATGTTACGAGACCTGTGTCATTCTC 199
DB 31 GlnuysGlnLeuIleCysProIleCysLeuGlnuMetPheThrLysProValIleLeu 50
QY 200 CTTGCCGACCAACTGTGTGAGGAAATGTGCGCATGATCTTTCAGGCTTAAACCG 259

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DB 51 ProCysGlnHi sAsnLeuCysArgLysCysAlaAsnAspIlePheGlnAlaSerAsnPro 70
QY 260 TACTTACCCACAAGAGAGGACACACCGTGGATCAAGGGGCGCTTCCGCTCC 319
DB 71 TyrLeuProThrArgGlyGlyThrThrMetAlaSerCylGlyArgPheArgCysProSer 90
QY 320 TGCACATGATGAGTGTGTTAAACAACATGGGGTCTATGACTGACAGAGAACTGCTC 379
DB 91 CysArgHisGlnValValIleuAspArgHisGlyValIleuIleuGlnuGlnuAsnLeuLeu 110
QY 380 GTGGAAACAATTATTTGATATCTAACAGCAGAA---TCCACCGAGCCAGAAAAAATTG 436
DB 111 ValGlnuSmIleIleAspIleTyrLysGlnGlnCysSerSerArgProLeuGlnuLysGly 130
QY 437 GACCAGCCCATGTGTGAAGACATGAAGAAGAACGATCAACATCTATTGTGTAAGTGT 496
DB 131 SerHisProMetCysLysGlnuHisGlnuAspGlnuLysIleAsnIleTyrCysLeuThrCys 150
QY 497 GAAGTCCCACTGTGTTCTTGTGCAAGGTTTGGCGCCCATTAAGACTGCGAGTGGCT 556
DB 151 GlnuValProThrCysSerMetCysLysValPheGlyIleHisLysAlaCysGlnuAla 170
QY 557 CCCCTGACTATGTGTTCCAGAGGACGAAGTCAAGCTCATGATGATGATGATGATGATCTT 616
DB 171 ProLeuGlnuSerValPheGlnuGlyGlnuLysThrGlnuLysuSmnLysCysIleSerMetLeu 190
QY 617 GTGGAGAACAGATAGAGTCCAGGGTGTGATGACGACGCTGGAGGACACCTGTAAACT 676
DB 191 ValAlaGlnuSmnAspArgValGlnuThrIleIleThrGlnuLysuSmnAspArgVal 210
QY 677 ATTGAGAGTGTGTCAGAAACGAAACGAGACCTGTGTGAAATTTGATCACTTATAC 736
DB 211 ThrLysGlnuSmnSerHisGlnuValLysGlnuLysuSerGlnuLysPheAspThrLeuTyr 230
QY 737 GGCATCGTGGAGAGAGATGAAATGACCAACGACCATCACTGAGAACAGAGAGAG 796
DB 231 AlaIleuAspGlnuLysLysSerGlnuLysuGlnuThrGlnuGlnuGlnuLys 250
QY 797 AAATCGAACATGTCCGAACTTATATCAAGAGATATTCGATCACTGAGAAAGTATCC 856
DB 251 LysLeuSerPheIleGlnuAlaLeuIleGlnuGlnuThrGlnuGlnuLysuSerThr 270
QY 857 AAGTTGTGATGATGAGAAATCCGATTCATGATGAGGCCCAAAATGCGAGATTTTCAG 916
DB 271 LysLeuValGlnuThrAlaIleGlnuSerLeuAspGlnuProGlyAlaThrPheLeuLeu 290
QY 917 AATGCCAAGACCCGTGTTGCAAAAAGATGTCGAAAGCATCAAAAGCGTTTCAGAGAGAA 976
DB 291 ThrAlaLysGlnuLeuIleLysSerIleValGlnuLysuSerLysCysGlnuLysGlyLys 310
QY 977 CTAGAACAGATTATGATCATGATGACCACTTCACTGTCATCTCAATAGAGAAAAA 1036
DB 311 ThrGlnuGlnuIleGlnuLeuMetAspPheThrLeuAspLeuHisIleAlaAsp 330
QY 1037 ATTATCCGTGAATAATTGACTTTTCTAGAGAAAGAGAAAGAGAAAGATGCAAGAAATA 1096
DB 331 AlaLeuArgAlaIleAspPheGlnuThrAspGlnuGlnuGlnuIleGlnuGlnu 350
QY 1097 GATGAAGAAGAGAAAGAGAGATGCACTGTAAGATGAAAGCAGAAATGTTCAATA 1156
DB 351 AspGlnu----- 353
QY 1157 GCATCTTCAGGGAGAGAGAGAGTGTGAGAAAGCTGACAGCCCTTCAG 1207
DB 354 -----GlnuGlnuLysuThrGlnuGlyLysGlnuGlnuIleGlnu 366

RESULT 13
US-10-061-043A-37
; Sequence 37, Application US/10061043A
; Publication No. US20030129686A1
; GENERAL INFORMATION:
; APPLICANT: Glaas, David
; APPLICANT: Bodine, Sue

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OM nucleic - nucleic search, using sw model

Run on: June 14, 2005, 16:12:56 ; Search time 1270 Seconds
(without alignments)
12072.543 Million cell updates/sec

Title: US-10-775-627A-3
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Sequence: 1 ctcgagattacccttacg.....ctccttccttccttcctcc 2590

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
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12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2590	100.0	2590	6	ABA99062 Murine mu
2	1266.4	48.9	1925	10	ADb62519 Human CDN
3	910.8	35.2	2434	8	AAAd9597 Human cyt
4	910.8	35.2	2634	10	ADb62279 Human CDN
5	910.8	35.2	2662	12	ADQ24315 Human scf
6	899.8	34.7	1762	4	AAAS2855 Human CDN
7	899.8	34.7	1762	8	ABX73196 Human nov
8	841.2	32.5	1426	10	ADc30799 Human nov
9	485.6	18.7	1757	6	ABs70380 Human bon
10	485.6	18.7	2110	5	AAAS42490 Human bon
11	461	17.8	1405	10	ADc30183 Human nov
12	461	17.8	1913	5	AAH68563 Human nov
13	461	17.8	1990	5	AAH78026 Human pro
14	452	17.5	1053	6	ABQ79506 Rat MURF1
15	450.8	17.4	1431	6	ABA99061 Murine mu
16	449.2	17.3	1349	3	AAA72433 Human nuc
17	440.8	17.0	2097	6	ABQ79507 Human MUR
18	439.2	17.0	1231	5	AAH90037 Human bon
19	439.2	17.0	1764	5	ABA83058 Human tra
20	439.2	17.0	1764	10	ADAS3654 Human cod

21	439.2	17.0	2700	12	ADQ24981	Adq24981 Human scf
22	436	16.8	1781	4	AAAS25842	AAAS25842 Human CDN
23	436	16.8	1781	8	ABX73183	ABX73183 Human nov
24	432.2	16.7	1597	8	ABA99063	ABA99063 Murine mu
25	419.4	16.2	867	6	ABQ79512	ABQ79512 Human MUR
26	376.6	14.5	573	10	ADc32553	ADc32553 Human nov
27	373.6	14.4	587	4	AAAS26314	AAAS26314 Human CDN
28	373.6	14.4	587	8	ABX73655	ABX73655 Human nov
29	361.4	14.0	1183	5	AAH90117	AAH90117 Human bon
30	344.8	13.3	1796	5	AAH89924	AAH89924 Human bon
31	344.4	13.3	2040	6	AAAS27653	AAAS27653 DNA encod
32	308.6	11.9	2040	6	ABN85313	ABN85313 Human cyt
33	288.2	11.1	630	6	ABQ79510	ABQ79510 Rat MURF1
34	285.2	11.0	498	9	ACH44808	ACH44808 Human fce
35	284	11.0	391	3	AACT5969	AACT5969 Human ORF
36	243.8	9.4	496	9	ACH15746	ACH15746 Human adu
37	241.8	9.3	531	3	AACT5285	AACT5285 Human ORF
38	241.8	9.3	531	6	ABN78104	ABN78104 Human int
39	206.6	8.0	2762	12	ADP22641	ADP22641 Sea-squid
40	167	6.4	424	9	ACH18104	ACH18104 Human adu
41	156.6	6.0	411	9	ACH17597	ACH17597 Human adu
42	151	5.8	446	4	AAAS26103	AAAS26103 Human CDN
43	151	5.8	446	8	ABX73644	ABX73644 Human nov
44	140.4	5.4	1039	6	ADd42866	ADd42866 Human DNA
45	140.4	5.4	1039	10	ADH62597	ADH62597 Human ven

ALIGNMENTS

RESULT 1
ABA99062
ID ABA99062 standard; DNA; 2590 BP.

AC ABA99062;
DT 15-JUL-2002 (first entry)

DE Murine muscle ring finger protein 2 (MURF-2) coding sequence.

KW Muscle ring finger; MURF-2; mouse; cardiac; microtubule;

KM intermediate filament; striated muscle; cardiac hypertrophy;

KW heart disease; gene; ds.

XX Mus musculus.

OS Mus musculus.
FH Key Location/Qualifiers

FT CDS /*tag= a
FT /product= "MURF-2"

XX WO200206318-A2.

XX 24-JAN-2002.

XX 18-JUL-2001; 2001WO-US022896.

XX 18-JUL-2000; 2000US-0219020P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Olson EN, Spencer JA;

XX WPI, 2002-241506/29.

XX DR P-PSDB; ABB08276.

XX Novel muscle ring finger protein useful for drug screening, and for
XX diagnosing and treating diseases, particularly cardiomyopathies.

XX Claim 4; Page 126-129; 134pp; English.

XX The sequence encodes murine muscle ring finger protein 2 (MURF-2). The
XX invention relates to a purified muscle ring finger (MURF) protein.

selected from MURF-1, MURF-2 and MURF-3. The MURF proteins of the invention are involved in microtubule and intermediate filament stabilisation of striated muscle cells and have cardiant activity. The MURF proteins are useful for screening a candidate substance for MURF protein-binding activity, in a cell, cell-free system or in vivo, and its effect on interaction of MURF with microtubules, homodimerisation of MURF, MURF-1, MURF-2 or MURF-3 stabilisation of microtubules, interaction of MURF with intermediate filaments, e.g. desmin, vimentin and cyokeratin, and heterodimerisation of MURF. The screened compounds are useful for treating and preventing cardiac hypertrophy and heart diseases. MURF proteins are useful as antigens to immunise animals for the production of antibodies

Sequence 2590 BP; 703 A; 627 C; 625 G; 635 T; 0 U; 0 Other;

Query Match 100.0%; Score 2590; DB 6; Length 2590;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCGAGATTTACCCCTTACAGAAAGCTGTCGGAGGACCTTCCCTTGGCAGACACTGAG 60
DB 1 CTCGAGATTTACCCCTTACAGAAAGCTGTCGGAGGACCTTCCCTTGGCAGACACTGAG 60
QY 61 GGCACGGGACGGCAAGAAATGAGCACTTCTGTAATTACAACTTTTCTCCAAAGACA 120
DB 61 GGCACGGGACGGCAAGAAATGAGCACTTCTGTAATTACAACTTTTCTCCAAAGACA 120
QY 121 GCAGACATGATTAAGTGAAGAAAGCACTGATCTGTCCCATCTGCGTAGAGATGTTAC 180
DB 121 GCAGACATGATTAAGTGAAGAAAGCACTGATCTGTCCCATCTGCGTAGAGATGTTAC 180
QY 181 GAAGCTGTGTGATCTTCCCTTGCAGACAAACCTGTGCAGAAATGTGCAGTGACAT 240
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QY 241 CTTCCAGGCTCTTAACCCGTAATTAACCAAGAGAGAGCACACCTGTGTCATGAGGGG 300
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DB 241 CTTCCAGGCTCTTAACCCGTAATTAACCAAGAGAGAGCACACCTGTGTCATGAGGGG 300
QY 301 CCGCTTCCGCTGTCCCTCTGACAGATGAGGTGTGTTAGACAGATGGGGTCTATGG 360
DB 301 CCGCTTCCGCTGTCCCTCTGACAGATGAGGTGTGTTAGACAGATGGGGTCTATGG 360
QY 361 ACTGCAGAGAACTGCTGTGTGAAAAATTATTTATTAACAAGAGAAATCCACCCAG 420
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QY 421 GCCAGAAAAAAATTGACACAGCCCATGTGTGAAAGACATGAAGAGAAACCATCAACAT 480
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QY 661 GGCACCTGTAAAACTATTGAGAGTGTGCGAGAAAGAGAAACGAGACTGTGTGAGAA 720
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QY 721 ATTGATCACTATACGGCATCTGTGAGAGAGAGAAAGCTGAATGATCCAGAGCATCAC 780
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QY 781 TCGAACAAGAGAGAAAGCTGGAACATGTCCGAACTCTTATCAGGAAGTATCCGATCA 840
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DB 781 TCGAACAAGAGAGAAAGCTGGAACATGTCCGAACTCTTATCAGGAAGTATCCGATCA 840
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DB 841 CTTGAGAAAGTATCCAAAGTTGTGAGAGTCAAGATTCAGTTGATGAGCCGAAAT 900
QY 901 GGCAGATTTTCTGAGAAATCCCAAGACCTGTGTCAAAGATGTGAGACATCAAGGC 960
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QY 1021 CAATGAGAGAAAGAAATTAATCCGTGAAATTTGACTTTTCTAGAGAGAGAGAGAGA 1080
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DB 1201 CTCTCAGCTTCCGACAGAGCTTCAAGGTGCGCCGACAGCCACTACTCTCTCCAGA 1260
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DB 1321 CATTTGCTCCAGAGACCAACAGTCTGAACCTTCAAGGCCCTTCAAGCCGGAACCTGC 1380
QY 1381 GGAATCCCTGTTTAACTCCCTAGTGTATTAAGGCCAAAGCCGGAACCAAGCTCAACCC 1440
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DB 1441 ACCTTGACATCATGAGAGTGAAGGTCTGGGTCAAAATGAGGCTCTGAGGCAATGAGATTG 1500
QY 1501 CAGTGTCACTCCGACAGAAATGTGCAAGGCCGAAACCAATGAGCAGCAGTGAATGG 1560
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DB 1621 GGGACAGTCTGACAGCTTGGGGAAGTGGGGGTGGGTATCTGAGCCAGCTGCGCAGTGC 1680
QY 1681 TTCTCCCTTCTCTGTTTGAATTCCTCAAAATGAATTAATTTATTTCTCCGTTGCTGCCCC 1740
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DB 1801 ATATGAAAGGAGACCTCTGACAGGATTTCTGAAAGCAAAACAAATATCAACACC 1860
QY 1861 ACCCTTTAATTCAGATGACTTATCTCACTCATTTGAGAAAAATGATTTGTCTCAAGACAAA 1920
DB 1861 ACCCTTTAATTCAGATGACTTATCTCACTCATTTGAGAAAAATGATTTGTCTCAAGACAAA 1920

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Dp	1921	ATTACAGAAAATACTCTCTGAAAGAACTTATCTTCGCAAACTTTCATTGCTGAG	1980
QY	1981	AAACCTTCTGAAGTTGTGTAGTGTGTGTGCATGCTGTGTATCAGCCATAGTGCAG	2040
Dp	1981	AAACCTTCTGAAGTTGTGTAGTGTGTGTGCATGCTGTGTATCAGCCATAGTGCAG	2040
QY	2041	TGTGTACAAAGTGGCAGAACACTGCCAGCTCCCTCAGGCTCTGTGTTATTTTAGAC	2100
Dp	2041	TGTGTACAAAGTGGCAGAACACTGCCAGCTCCCTCAGGCTCTGTGTTATTTTAGAC	2100
QY	2101	GCTTGTGCGCTTTTGCCTTTCTCCTTAGCAATTGCAGTGTAGTGTATGTTCACTGTCAGT	2160
Dp	2101	GCTTGTGCGCTTTTGCCTTTCTCCTTAGCAATTGCAGTGTAGTGTATGTTCACTGTCAGT	2160
QY	2161	TTCGAAACTGACCCGATTTATGCAAAATATAGAGAAATGTGTACATGACCAAGCTATGTAGGC	2220
Dp	2161	TTCGAAACTGACCCGATTTATGCAAAATATAGAGAAATGTGTACATGACCAAGCTATGTAGGC	2220
QY	2221	ACTGTAGAGGTTCCCTTCCCTATGAGATGCGATGGGTGGCAGACAGACTTTCCTTTACA	2280
Dp	2221	ACTGTAGAGGTTCCCTTCCCTATGAGATGCGATGGGTGGCAGACAGACTTTCCTTTACA	2280
QY	2281	TGTGGCCACACGTGCATATGTCAAGAGGCCAAAATCTAGGGCAACTTTTGTGACATTTT	2340
Dp	2281	TGTGGCCACACGTGCATATGTCAAGAGGCCAAAATCTAGGGCAACTTTTGTGACATTTT	2340
QY	2341	TCTAACCTTATTTACATATCTCATTAATCATATCCATGTATTAGGATTTTAAATGGAATTT	2400
Dp	2341	TCTAACCTTATTTACATATCTCATTAATCATATCCATGTATTAGGATTTTAAATGGAATTT	2400
QY	2401	CAAGAGAGAGCTGTCTACTTCTTTAAGTGTCTGTGCATAGCAGAGAACTGTAAATCTGTG	2460
Dp	2401	CAAGAGAGAGCTGTCTACTTCTTTAAGTGTCTGTGCATAGCAGAGAACTGTAAATCTGTG	2460
QY	2461	GAGGAACTGACATGATTTAAAGTATATACACAATCTCCCCGATGTGCTTCTCATCTC	2520
Dp	2461	GAGGAACTGACATGATTTAAAGTATATATACACAATCTCCCCGATGTGCTTCTCATCTC	2520
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QY	2581	TTCTTCTCTCC 2590	
Dp	2581	TTCTTCTCTCC 2590	

RESULT 2
ID ADB62519
ADBB62519 standard; cDNA; 1925 BP.
AC ADB62519;
XX 04-DEC-2003 (first entry)
DE Human cDNA encoding clone HEART20019310.
KW Human; sex; gene; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related oporosis; neurological disease; cancer; tumour.
OS Homo sapiens.
FT Key Location/Qualifiers
CDS 47..1693
FT /*tag= a
/product= "Clone HEART20019310 protein"
EP1308459-A2.

PD	XX		07-MAY-2003.
PF	XX		28-MAR-2002; 2002EP-00007401.
PR	XX		05-NOV-2001; 2001JP-00379298.
PR	XX		25-JAN-2002; 2002US-00350978.
PA	XX	(HELI-) HELIX RES INST.	
PA	XX	(REAS-) RES ASSOC BIOTECHNOLOGY.	
XX	XX	Iscgai T, Sugiyama T, Ocsuki T, Wakamatsu A, Sato H, Ishii S,	
P1	XX	Yanamoto Y, Isono Y, Hio Y, Otsuka K, Nagai K, Itie R, Tamechika I,	
P1	XX	Seki N, Yoshikawa T, Otsuka M, Nagahari K, Maubo Y;	
DR	XX	WPI: 2003-450961/43.	
DR	XX	P-PSTD: ADB64489.	
PT	XX	New polynucleotides and polypeptides, useful for developing a diagnostic	
PT	XX	marker or medicines for regulation of their expression and activity, or	
PT	XX	as targets of gene therapy.	
PS	XX	Claim 1; Page: 222pp; English.	
CC	XX	The invention discloses a polynucleotide comprising a sequence selected	
CC	XX	from 1970 fully defined nucleotide sequences which encode novel	
CC	XX	polypeptides. Also claimed is a polypeptide encoded by the polynucleotide	
CC	XX	or its partial peptide, an antibody binding to the polypeptide or peptide	
CC	XX	of the polynucleotide, immunologically assaying the polypeptide or	
CC	XX	peptide of the polynucleotide by contacting the polypeptide or peptide	
CC	XX	with the antibody of the encoded protein, and observing the binding	
CC	XX	between the two, a transformant carrying the polynucleotide in an	
CC	XX	expressible manner and an antisense polynucleotide. The oligonucleotide	
CC	XX	is useful as a primer for synthesising the polynucleotide, or as a probe	
CC	XX	for detecting the polynucleotide. The polynucleotides and encoded	
CC	XX	proteins are useful as pharmaceutical agents and many disease-related	
CC	XX	genes may be included in them, for developing a diagnostic marker or	
CC	XX	medicines for regulation of their expression and activity, or as targets	
CC	XX	of gene therapy. The genes are involved in tissue and/or cell	
CC	XX	regeneration. Membrane proteins, signal transduction-related proteins,	
CC	XX	transcription-related proteins, disease-related proteins and genes	
CC	XX	encoding them can be used as indicators for diseases (e.g. osteoporosis,	
CC	XX	neurological diseases, cancer, tumours). The cDNA may be used to regulate	
CC	XX	the activity or expression of the encoded protein to treat diseases. The	
CC	XX	sequence presented is a cDNA of the invention. Note: Some of the sequence	
CC	XX	data for this patent is not represented in the printed specification, but	
CC	XX	is based on sequence information supplied by the European Patent Office.	
XX	XX	Sequence 1925 BP; 579 A; 441 C; 498 G; 407 T; 0 U; 0 Other;	
SO	XX		
		Query Match	48.9%; Score 1266.4; DB 10; Length 1925;
		Best Local Similarity	82.0%; Pred. No. 0;
		Matches 1571; Conservative	0; Mismatches 301; Indels 44; Gaps 8;
Oy	GGGACGGCAAGGAATGAGCACTTCGTGAATTACAAGTCTTTGCCAAGAGCAGAGA	125	
Dd	GGGACGGCAAGGAATGAGCACTTCGTGAATTACAAGTCTTTGCCAAGAGCAGAGA	92	
Oy	126 CCATGATAACTTGAAAGAACCACTGATCTGTCCCATCTGCCTTAGAGATGTCAGAAC	185	
Dd	93 CCATGATAACTTGAGAGAGCACTCATCTGTCCCATCTGCTTGAAGATGTCAGAAAC	152	
Oy	186 CTGTGTGTCATTTCTCCCTTGGCCAGCAACCCTGTGCAGAAAATGTGCCAGTGAACATTTCC	245	
Dd	153 CTGTGTGTCATTTCTCCCTTGTGAGCAACCTGTGTAGAAAATGTGCCAGTGAATTTTTCC	212	
Oy	246 AGGCGCTTAACCCGCTACTTACCCCAAGAGGAGCACCAACGCTGGCATCAAGGGGCGCGT	305	
Dd	213 AGGCGCTTAACCGGTATTTGGCCCAAGAGGAGGTACCAACATGAGCATCAAGGGGCGCAT	272	
Oy	306 TCAGCTGTCTCTCTCTGACAGACATGAGGTGTGTAGACAGACATGGGGTCTATGACATCGC	365	
Dd	273 TCAGCTGTCTCTCTCTGAGACATGAGGTGTGTGTAGACATGAGGGGTATATGACATTCG	332	

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OY 366 AGAGAACTGCTCTGTGAAAAACATTATTGATATCTACAGAGGAATCCACGAGCCAG 425
DB 333 AGAGAACTGCTGTGTGAAAAATATCATTTGACATCTACAGAGGAGTCCACGAGCCAG 392
OY 426 AAAAAAATTTGACCAAGCCCATGTGTGAAGCATGAAGAGAAAGCATCAACATCTATT 485
DB 393 AAAAAAATTCGACCGACCATGTGTGAGAAACATGAAGAGAGGCGATCAACATCTACT 452
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DB 453 GTCTGAATGTGGAATACCCACTGTCTCTGTGTGAAGTGTGTGTGTCAACAAAGACT 512
OY 546 GCGAGTGGCTCCCTGACTCATGTGTTCAGAGGAGAACTCAGAGCTCAGATGTGTA 605
DB 513 GCGAGTGGCTCCCTCCTCATGTGTTCAGAGACAGAACTGTGAGTCTGAGTGTGCA 572
OY 606 TTGCTGTCTGTGTGGAAGCAACGATAGAGTTCAGAGGTGTGTATCAGCCAGCTGAGAGCA 665
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OY 666 CCTGTAAAACTATTGAGAGTGTCTGAGAAAGCAGAAACAGGACCTGTGTGAGAAATTG 725
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OY 726 ATCACTATACGGCATCTGTGAGAGAGAGAAAGACTGAATGACCCAGCCATCACTCGAA 785
DB 693 ATTACTGTATGTGCAATTTTGGAGGAGAGAAATGAATGACCCAGTCAATTACCGAA 752
OY 786 CACAGAGAGAGAACTGGAACATGTCCGAATCTCTTATCAGAAAGTATTCGATCACTCG 845
DB 753 CCAAGAGAGAGAACTGGAACATGTCCGTCTGTATCAAAAGATTCATGATCTTATTTG 812
OY 846 AGAAGTATCCAAAGTGTGTGAGTCAAGGATCCAGTTCATGAGTGTGAGCCGAGAAATGCGAG 905
DB 813 AGAAGTCTCAAGTGTGTGTGAGTCAAGGATTCAGTTCATGAGTGTGAGCCAGAAATGCGAG 872
OY 906 TATTTCTGAGAAATGCGAAGACCCCTGTTCAAAAGATGTGGAAGCATCAAGGCGTTTC 965
DB 873 TGTTCCTGCAAAATGCCAAACCCCTGTAAAAAAATCTCGAAGCATCAAGGCAATTTC 932
OY 966 AGATGAGAAATCTGAAACAAAGTTATGATCATGAGCACTTCACTGTCAATCTCAATA 1025
DB 933 AGATGAGAAATATGAAACATGCTATGAGAACATGAAACACTTCACTCACTCATATA 992
OY 1026 GAGAAAGAAAAATTAATCCGTGAATTTGACTTTTCTAGAGAGAGAGAGAGAGAGATG 1085
DB 993 GAGAAAGAAAAATTAATACGTGAATTTGACTTTTCAAGAGAGATGAAGTGAAGAGAG 1052
OY 1086 CAGAGAAATGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1130
DB 1053 AAGAAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1112
OY 1131 TAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1190
DB 1113 TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1172
OY 1191 CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1250
DB 1173 CTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1226
OY 1251 CTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1310
DB 1227 CTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1286
OY 1311 AGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1370
DB 1287 AGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1346
OY 1371 CGAGAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1430
DB 1347 CGAGAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1406

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OY 1431 GCTCCAAACCACTTGACATCATGAGAGTGAAGCTGTGGTCAAAATAGGCTCTGAGCA 1490
DB 1407 CCACGAACCCACCTTGACATCCCAAGGAGGAGAGAGTCTGGGGCAAAATAGGCTCTGAGCA 1466
OY 1491 TTGAGATTTCAAGTGTGCACTCCGCAAGTGGCAGAAAGCCGCAACCAATGACAGGCA 1550
DB 1467 CTGAGATTTGAAATGTACGGAAGGCAAGTGGCAGAGCCGAGCGAGAGAGAGGCA 1526
OY 1551 CAGTGAAGTGAAGAGTCTAGTTCAACCTGACACTACTCTCAGATTTGAGAGCC 1610
DB 1527 CTGAGATTTGAAAGAACTAGTGCACCTGACACTACTCTCAGATTTGAGAGCTC 1586
OY 1611 CTTCTCCAGAGAGCACTCTGACAGCTTGGGAGTGGGGGTGG- GGTGATCTGAGCCAG 1669
DB 1587 CTCCTCTCAGAGAGCAAGCTGACAGCTCAGCGAGTGGCAGTGAATTTGAGCCAG 1646
OY 1670 CTGCGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1729
DB 1647 CTGCGCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1705
OY 1730 TTGCTGCCCC-CTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1788
DB 1706 CTGCTGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1765
OY 1789 TCACACGATTC--TATGAAGGAGACTCTGAGACAGATTTCTGAAACCAAAACAAA 1845
DB 1766 TTAATATTATGACAGATGATGAAGAGGACCTGTAACAGAGATTTCTGCA----- 1813
OY 1846 CAATACACACCAACCCCTTAATTCAGATGATGATGATGATGATGATGATGATGATGAT 1904
DB 1814 ----AAATATGCCCCCAATGCAATTCATATGATGATGATGATGATGATGATGATGAT 1869
OY 1905 TTAATGCTCAGACAAATTAACAGAAATTAATCTCTGAAAGAACTTGATCTGCTGC 1960
DB 1870 ATATTGTAAGAAATAGTTGACAGAAAGCACTGAAATTAATTAACCTTGATCTTATAC 1925

RESULT 3
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ID AAD49597 standard; cDNA; 2434 BP.
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AC AAD49597;
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XX 24-MAR-2003 (first entry)
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DE Human cytoskeleton-associated protein, CSAP-8 cDNA.
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XX Human, cytoskeleton-associated protein; CSAP-8; atherosclerosis; cancer;
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XX gene therapy; gene; ss.
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XX Homo sapiens.
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XX CDS 184..1542
XX FT /*tag= a
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XX MO200279404-A2.
XX
XX PD 10-OCT-2002.
XX
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XX 25-MAR-2002; 2002MO-US009288.
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XX 29-MAR-2001; 2001US-0280508P.
XX 03-APR-2001; 2001US-0281323P.
XX 13-APR-2001; 2001US-0283769P.
XX 04-MAY-2001; 2001US-0288609P.
XX 10-MAY-2001; 2001US-0290518P.
XX 18-MAY-2001; 2001US-0291870P.
XX 29-MAY-2001; 2001US-0294451P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX

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PI Hafalia AJA, Tang TY, Yue H, Khan FA, Ison CH, Baughn MR;
 PI Warren BA, Duggan BM, Thangavelu K, Honchell CD, Azimzai Y;
 PI Elliott VS, Burford N, Ding L, Yue H, Becha S, Emetzel EM;
 PI Richardson TW, Lee ST, Bandman O, Lai PG, Lee S, Gietzen KJ;
 PI Walla NK, Griffin JA, Lee EA, Swarnakar A, Ring HZ, Jones KA;
 DR WPI: 2003-092894/08.
 P-PSDB; AAE32110.

PS New human cytoskeleton-associated proteins, useful for preparing a
 PT composition for diagnosing or treating a disease or condition associated
 PT with decreased expression or overexpression of functional CSAP e.g.,
 cancer.

XX Claim 5; Page 211-212; 233pp; English.

XX The invention relates to new human cytoskeleton-associated protein (CSAP)
 CC and its polynucleotide. The polypeptide is useful for preparing a
 CC composition for diagnosing or treating a disease or condition associated
 CC with decreased expression or overexpression of functional CSAP e.g.,
 CC atherosclerosis or cancer. The present sequence is human CSAP-8 cDNA. The
 CC invention is useful in gene therapy

SO Sequence 2434 BP; 753 A; 511 C; 553 G; 617 T; 0 U; 0 Other;

Query Match 35.28; Score 910.8; DB 8; Length 2434;
 Best Local Similarity 84.28; Pred. No. 1e-231;
 Matches 1058; Conservative 0; Mismatches 177; Indels 21; Gaps 2;

QY 66 GGGACGGCAAGAAATGAGCACTTCTGAATTACAGTCTTTTCCAAAGAGAGAGA 125
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 QY 306 TCCGCTGTCCCTCTGACAGATGAGGTGTGTAGACAGACATGGGGTCTATGACTGC 365
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 DB 710 TTGCTGACTTGTGGAGAGCAAGATAGATCCAGGGTGTGTAGCAGCTGTGAGAAATTTG 769
 QY 666 CTGTGAAATCTATTGAGAGAGTGTGCAAGAAAGCAAGAACTGTGTGAGAAATTTG 725
 DB 770 CTGTGAAATCTATTGAGAGAGTGTGCAAGAAAGCAAGAACTGTGTGAGAAATTTG 829

QY 726 ATCACTTATCGGCATCTGAGAGAGAGAGAACTGAATGACCCAGGCATCACTCGAA 785
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 QY 786 CACAGAGAGAGAACTGGAACATGTCCGAATCTTTATCAGAGAAATTCGATCACCAG 845
 DB 890 CCCAAGAGAGAGAACTGGAACATGTCCGATCTGTATCAAAAAGTATTCATCATTTGG 949
 QY 846 AGAAGCTATCCAGTGTGTGAGTCAAGATTCAGTTCATGATGAGCCGAAATGGCAG 905
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 DB 1190 AGAAG 1249
 QY 1131 TAGAAG 1190
 DB 1250 TGGAG 1309
 QY 1191 CTGAG 1250
 DB 1310 CTGAG 1363
 QY 1251 CCTCTCAG 1306
 DB 1364 CCTCTCAG 1419

RESULT 4
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 ID ADB62279 standard; cDNA; 2634 BP.
 AC ADB62279;
 DT 04-DEC-2003 (first entry)
 DE Human cDNA encoding clone DPNES20073320.
 KW Human; ss; gene; pharmaceutical; diagnostic; gene therapy;
 KW tissue regeneration; cell regeneration; membrane protein;
 KW signal transduction-related protein; transcription-related protein;
 KW osteoporosis; neurological disease; cancer; tumour.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 377..1735
 FT /tag= a
 FT /product= "Clone DPNES20073320 protein"
 PN EPI308459-A2.
 PD 07-MAY-2003.
 PE 28-MAR-2002; 2002EP-00007401.
 PR 05-NOV-2001; 2001JP-00379298.
 PR 25-JAN-2002; 2002US-00350978.
 PA (HELI-) HELIX RES INST.

XX WO200155322-A2.
PR 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US001341.
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
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PR 01-DEC-2000; 2000US-0250391P.
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PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX

PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-48873/53.
 DR P-PSDB; AAU5866.
 XX
 PT New nucleic acid molecules encoding 461 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives.
 XX
 PS Claim 1; SEQ ID NO 34; 980bp; English.
 CC
 CC The invention relates to isolated nucleic acid molecules and their
 CC encoded secreted proteins. The nucleic acids and proteins are used to
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
 CC in diagnosing a pathological condition or susceptibility to a
 CC pathological condition. Antibodies to the proteins can also be used in
 CC alleviating symptoms associated with the disorders and in diagnostic
 CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
 CC (ELISA). Disorders which are diagnosed or treated include autoimmune
 CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
 CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
 CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angioneu-
 CC rous system disorders e.g. Alzheimer's disease, infections caused by
 CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
 CC and many other disorders listed in the specification. The polypeptides
 CC can also be used to aid wound healing and epithelial cell proliferation,
 CC to prevent skin aging due to sunburn, to maintain organs before
 CC transplantation, for supporting cell culture of primary tissues, to
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used
 CC as a food additive or preservative to increase or decrease storage
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
 CC minerals, cofactors and other nutritional components. The present
 CC sequence encodes a novel secreted protein of the invention. Note: The
 CC sequence data for this patent did not form part of the printed

Query Match 34.7%; Score 899.8; DB 4; Length 1762;
 Best Local Similarity 84.2%; Pred. No. 7.6e-229;
 Matches 105; Conservative 0; Mismatches 177; Indels 22; Gaps 3;

QY 66 GGGAGCGGCAAGAAATGAGCACTTCTGAAATTACAGTCTTTCTCCAAAGACAGAGA 125
 DB 143 GGGAGCGGCAAGAGATAGCGCATCTCTGAATTACAAATCTTTTCCAAAGACAGAGA 202
 QY 126 CCATGTAATCTGGAAGAAAGCACTGCTGCCATCTGCTAGATTTTCAACGAGC 185
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 DB 563 TGTCTGAATCTGTAAGTGGCCACTGTTCTCTGTGCAAGGTTTTTGGCGCCCATAGAG 622
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 DB 983 GTGTTTCTGAGAAATGCAAGACCTGTTGCAAAAGATGTGAGAGCATCAAGGCGATT 1042
 QY 965 CAGATGAGAAATATGAAACAGATGATGATGATGATGATGATGATGATGATGATGAT 1024
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RESULT 7
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 ID ABX73196 standard; DNA; 1762 BP.
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 AC ABX73196;
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 DT 18-MAR-2003 (first entry)
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 DE Human novel polynucleotide #24.
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 KM Human; gene; de; neural disorder; immune system disorder; renal disorder;
 KM muscular disorder; respiratory disease; reproductive disorder;
 KM gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
 KM hyperproliferative disorder; inflammatory disease; allergic reaction;
 KM blood related disorder; cancer; immunosuppressive; anti-inflammatory;
 KM cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;
 KM haemostatic; antihistaminic; antidiabetic.
 XX
 OS Homo sapiens.
 XX
 PN US2002132753-A1.

QY	845	NAGAAACGATCCAAAGTTGTTGAGATCAGAAATCCAGTTCAATGATGAGGCCGAATGCA	904
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QY	965	CAGATGGAGAAACTTNGAACAAGGTTATAGATCATGAGCACTTCACCTGTCAATCTCAAT	1024
Db	1043	CAGATGGAGAAATTTGAAACATGGCTTGTAGAACCACTTCCACGTCAACCTCAAT	1102
QY	1025	AGAGAGAAAAAATATATCCGTGAAATTGACTTTTCTAGAGAGAGAAAGAGAAAGAT	1084
Db	1103	AGAGAGAAAAAGATATATACGTGAATTTGACTTTTACAGAGAAAGATGAAGAAGAAAGCA	1162
QY	1085	GCAGAGAAATATGATGAAGAGAGAGAGACA-----GGATGCATGACAA	1129
Db	1163	GAAAGAACGCGAGAGAAAGAGAAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAA	1222
QY	1130	GTAGAGAGGCGAGAAATGTTCAATATACATCTTCAGGGGAAGAGAGAGATCTGAGAAA	1189
Db	1223	GTGGAAGAGGTGAGAAATGTTCAACACAGTTTCCAGAGAGAGAGTGAAGAACCCAGAAA	1282
QY	1190	GCTGCAGAGCCCTCTCAGCTTCCGCGACAGGCTTCAGTGTGCGCCAGAGCCACTACCTGCT	1249
Db	1283	GCTTCAGAGCTCTCTCAG-----GTGAGGTGACAGCGTGCCCTCGGGGCACTTCCAGTT	1336
QY	1250	TCTCTTCAGAAACCGTTTTCATCCATGCGACCTGTGTCAGATATGTCCTGTGTACACAG	1306
Db	1337	TCCTCTTCAGAGCCACCTCCAGCCCTGCGACCTGTGTGAGATGCCCTGTATACAG	1393

RESULT 8	
ADCC30799	
ID	ADCC30799 standard; cDNA, 1426 BP.
XX	
AC	ADCC30799;
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	Human novel cDNA sequence, SEQ ID NO:881.
XX	
KW	Human; diagnostic; drug screening; forensics; gene mapping;
KW	biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KM	neurodegenerative diseases; anemia; platelet disorder; wound; burns;
KW	ulcers; osteoporosis; autoimmune disease; cancer;
KM	molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW	neuroprotective; anti-anemic; anticoagulant; thrombolytic; vulnerary;
KM	antulser; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW	gene therapy; chromosome 8q13; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO2003029271-A2.
XX	
PD	10-APR-2003.
XX	
PF	24-SEP-2002; 2002MWO-US030474.
XX	
PR	24-SEP-2001; 2001US-0324631P.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
PI	Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
PI	Haley-Vacente D, Drmanac RT;
XX	
DR	WPI: 2003-371981/35.
XX	
DR	P-PSDB; ADCC31770.
XX	
PT	New polynucleotide and polypeptide useful for diagnosing, preventing or
PT	treating conditions such as neurodegenerative diseases, anemias, platelet

PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
 PT cancer.
 XX Claim 1, SEQ ID NO 881, 1185bp, English.
 PS

The invention relates to 971 novel human cDNA sequences (ADCC293919-ADCC30869) and the polypeptides they encode (ADCC30850-ADCC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; a method of detecting polynucleotides or polypeptides of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of preventing, treating or ameliorating a medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention; methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 coding sequences corresponding to the cDNA sequences of the invention (ADCC31861-ADCC32627) and the polypeptides encoded by the cDNAs (ADCC32628-ADCC33994). The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, anaemia, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human cDNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIP0 at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

SQ Sequence 1426 BP; 448 A; 320 C; 365 G; 293 T; 0 U; 0 Other;

Query Match 32.5%; Score 841.2; DB 10; Length 1426;

best local similarity 02.78; fixed: NO. 2.35-213;
Matches 1012; Conservative 0; Mismatches 178; Indels 34; Gaps 3;

Matches 1012; Conservative 0; Mismatches 178; Indels 34; Gaps 3;

QY 66 GGGACGGCAAGGAATGAGCACTTCTGAATTACAAGTCTTCTCCAAAGAGCAGCAGA 125

Db 120 GGACAGCGAGGAGATGAGCGCATCTCTGAATTACAATCTTTTCCAAAGAGCAGCAGA 179

126 CCATGATACTTGGAAAAGCACTGATCTGTCCCATCTGCCCTAGAGATGTTCAAGAAC 185

Db 180 CCATGATACTTAGAGAGCAACTCATCTGTCCCATCTGCTTAGAGATGTTCAAGAAC 239

186 CTGTGTCATTCTCCCTTGCAGCACCAACCTGTGCAGGAATGTGCCAGTGACATCTTC- 244

240 CTTGCTGATTCTCCCTTGTTCAGCACAACTGTGTAGGAATGTGCCAGTGATATTTTCC 299

My 245 -----CAGGCACTTAAACCCGTAATTAACCAACAAGAGAGCAACCAACCGTAGGCATTACG 296

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300 ACCCTGCGACCCCTTTTCCAGCAGCAATGCCTAC 359

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21

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2005, 19:51:42 ; Search time 7464 Seconds
(without alignments)
13208.261 Million cell updates/sec

Title: US-10-775-627A-3
Perfect score: 2590
Sequence: 1 ctcgagattacccttacag.....ctccttctctctctctcc 2590

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss81:*
9: gb_gss82:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	655.8	25.3	741	3	AK052918	AK052918 Mus muscu
2	624	24.1	822	5	BX427830	BX427830 BX427830
3	610.6	23.6	694	2	BB520266	BB520266 BB520266
4	565.2	21.8	790	4	BG674823	BG674823 BG674823
5	529.6	20.4	826	7	CK599151	CK599151 AGENCOURT
6	521.4	20.1	672	2	BB662321	BB662321 BB662321
7	508.2	19.6	647	7	CV026849	CV026849 4912 Full
8	494.6	19.1	657	7	CR754151	CR754151 CR754151
9	483.4	18.7	827	5	BUI131273	BUI131273 603116770
10	483.2	18.7	927	5	BUI29677	BUI29677 CR755417
11	480.6	18.6	655	7	CR755417	CR755417 CR755417
12	457.4	17.7	1077	9	AY411684	AY411684 Homo sapi
13	457	17.6	699	5	EX501677	EX501677 DKFZP779F
14	445.8	17.2	1161	4	BG163322	BG163322 602338256
15	442.4	17.1	1083	4	AY411686	AY411686 Mus muscu
16	441.2	17.0	840	5	BUI321841	BUI321841 603485910
17	441.2	16.9	991	5	AY411685	AY411685 Pan trogl
18	432.6	16.7	697	5	BUI45004	BUI45004 603229155
19	422	16.3	983	2	BF205857	BF205857 601868260
20	416.8	16.1	1092	4	BUI14696	BUI14696 602861723
21	413.2	16.0	1081	2	BF309583	BF309583 601891901
22	409.4	15.8	776	4	BUI14212	BUI14212 602862572
23	406.8	15.7	506	1	AA840584	AA840584 vnt77h09.r
24	404.6	15.6	657	7	CO506878	CO506878 GGEZEB201

25	390.8	15.1	684	7	CO506307	CO506307 GGEZEB101
26	380	14.7	828	7	CO506630	CO506630 GGEZEB101
27	377.6	14.6	612	7	CR439377	CR439377 CR439377
28	376.6	14.5	573	1	AA443443	AA443443 zw94c05.r
29	373.6	14.4	615	4	BU033623	BU033623 BU033623
30	361.2	13.9	751	6	CA342294	CA342294 672134 NC
31	361.2	13.9	775	7	CF290486	CF290486 AGENCOURT
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33	354.6	13.7	580	5	BP258248	BP258248 BP258248
34	350.8	13.5	647	7	CO506888	CO506888 GGEZEB201
35	350.6	13.5	800	5	BU220426	BU220426 603756441
36	349.8	13.5	786	7	CF289491	CF289491 AGENCOURT
37	349	13.5	900	5	BU266226	BU266226 603505103
38	348	13.4	1142	5	BU470941	BU470941 603363447
39	347.8	13.4	1455	3	CR677834	CR677834 Tetradon
40	346.8	13.4	797	7	CK697380	CK697380 ZF101-P00
41	344	13.3	890	5	BU107891	BU107891 603111441
42	342.8	13.2	614	7	CF615149	CF615149 CES008971
43	333.8	12.9	1466	3	CR670382	CR670382 Tetradon
44	333	12.9	966	5	BU135007	BU135007 603119195
45	332.8	12.8	952	5	BU241018	BU241018 603323733

ALIGNMENTS

RESULT 1
AK052918
LOCUS
DEFINITION
AK052918 741 bp mRNA linear HTC 03-APR-2004
Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched library, clone:DB3004C10 product:hypothetical RING finger /B-box zinc finger domain containing protein, full insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AK052918
AK052918.1 GI:26343090
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

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AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
Shibata,K., Itoh,M., Aizawa,K., Nagaoaka,S., Sasaki,N., Carninci,P., Kono,H., Akiyama,J., Nishi,K., Katsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujisake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

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TITLE
JOURNAL
MEDLINE
PUBMED
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 741)

ADACHI,J., AIZAWA,K., AKIMURA,T., ARAKAWA,T., BONO,H., CARNINCI,P.,
FUKUDA,S., FURUO,M., HANAGAKI,T., HARA,A., HASHIZUME,W.,
HAYASHIDA,K., HAYASHI,N., HIRAMOTO,K., HIRAKAWA,T., HIRAZANE,T.,
HORI,F., IMOTANI,K., ISHII,Y., ITOH,M., KAGAWA,I., KASUKAWA,T.,
KATO,H., KAWAI,J., KOJIMA,Y., KONDO,S., KONNO,H., KUNDA,M.,
KOYA,S., KURIHARA,C., MATSUYAMA,T., MIYAZAKI,A., MURATA,M.,
NAKAMURA,M., NISHI,K., NOMURA,K., NUMAZAKI,R., OHNO,M., OHSETO,N.,
OKAZAKI,Y., SAITO,R., SAITOH,H., SAKAI,C., SAKAI,K., SAKAZUME,N.,
SANO,H., SASAKI,D., SHIBATA,K., SHINAGAWA,A., SHIRAKI,T.,
SOGABE,Y., TAGAMI,M., TAGAWA,A., TAKAHASHI,F., TAKAHASHI,A.,
TAKEDA,Y., TANAKA,T., TOMARU,A., TOYA,T., YASUNISHI,A.,
MURAMATSU,M. and HAYASHIZAKI,Y.

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
Location/Qualifiers

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/db_xref="PANTOM:DB:D830041C10"
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ORIGIN

Query Match 25.3%; Score 655.8; DB 3; Length 741;
Best Local Similarity 99.7%; Pred. No. 1.1e-16;
Matches 657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 12 CCCTTACAGAACTGTTGGAGGACCTTTCCTTGGAGAGACCTCAGGAGAGGAGCG 71
Db 83 CACTTACAGAAAGCGTTTGGAGGACCTTTCCTTGGAGGACCTCAGGAGAGGAGCG 142
Qy 72 GCAAGAAATGAGCACTTCTGGAATTCAAGTCTTTTCCAAAGAGAGAGACCATGG 131
Db 143 GCAAGAAATGAGCACTTCTGGAATTCAAGTCTTTTCCAAAGAGAGAGACCATGG 202
Qy 132 ATAACCTGGAAGCACTGATCGTCCCATCTGCTGAGAGATTTTCAAGAGCTGTGG 191
Db 203 ATAACCTGGAAGCACTGATCGTCCCATCTGCTGAGAGATTTTCAAGAGCTGTGG 262

Qy 192 TCATTCTCCCTTGGCAGACACAACTGTGAGAAATGTGCCAGTGCATCTTCAGGCT 251
Db 263 TCATTCTCCCTTGGCAGACACAACTGTGAGAAATGTGCCAGTGCATCTTCAGGCT 322
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Db 323 CTAAACCCGTAATCCCAAGAGAGAGCACCACCTGGCATCAGGGGGCCGCTTCCGCT 382
Qy 312 GTCCCTCTGAGACATGAGGTGGTGTTAACAAGACATGGGGTCTATGACTGAGAGGA 371
Db 383 GTCCCTCTGAGACATGAGGTGGTGTTAACAAGACATGGGGTCTATGACTGAGAGGA 442
Qy 372 ACCTGCTGTGGAAGAAACATTATTGATATCTTCAAGCAGAGATCCACGAGCCAGAAAAA 431
Db 443 ACCTGCTGTGGAAGAAACATTATTGATATCTTCAAGCAGAGATCCACGAGCCAGAAAAA 502
Qy 432 AATTGACACAGCCCATGTGTGAAAGAGCATGAAGAACCATCATACATCTATTGTCTGA 491
Db 503 AATTGACACAGCCCATGTGTGAAAGAGCATGAAGAACCATCATACATCTATTGTCTGA 562
Qy 492 ACTGTGAAGTGCACCTGTTCCTTGTGCAAGGTTTTGGCGCCATTAAGACCTGCAGG 551
Db 563 ACTGTGAAGTGCACCTGTTCCTTGTGCAAGGTTTTGGCGCCATTAAGACCTGCAGG 622
Qy 552 TGGCTCCCTGACTCATGTGTTCAGAGGAGAGTCAAGCTCATGTGATGTATGCTG 611
Db 623 TGGCTCCCTGACTCATGTGTTCAGAGGAGAGTCAAGCTCATGTGATGTATGCTG 682
Qy 612 TACTTGTGGAGAGCAAGATAGTCCAGGGTGTGATCAGCCAGCTGTGAGAGCACTGT 670
Db 683 TACTTGTGGAGAGCAAGATAGTCCAGGGTGTGATCAGCCAGCTGTGAGAGCACTGT 741

RESULT 2
BX427830 822 bp mRNA linear EST 05-MAY-2004
LOCUS
DEFINITION
BX427830 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
CS0DM012YM10 5-PRIME, mRNA sequence.
ACCESSION
BX427830
VERSION
BX427830.2 GI:47037092
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 822)
Li,W.-B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30788679.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequenage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 4738.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DM012B05QP1&c=4738.f.

FEATURES
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/note="Organ: liver; Vector: pCMVSPORT_6; 1st strand cDNA

prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCTCGATTATTAATTAATCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified Bluescript KS(+) after bulk excision from Lambda FLX I."

ORIGIN

Query Match 23.6%; Score 610.6; DB 2; Length 694;
Best Local Similarity 98.1%; Pred. No. 9.7e-150;
Matches 628; Conservative 0; Mismatches 10; Indels 2; Gaps 1;

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DB 57 GGAGACACTTTTCTTGGCAGACACCTGAGGAGAGGAGCGGCAAGAAATGAGACTCT 116
QY 91 TCTGAATTAACAAGCTTTCTCCAAAGAGCAGACCACTGATTAATCTGGAAAAACAAC 150
DB 117 TCTGA--TMACAGCTTCTCCAAAGAGCAGACCACTGATTAATCTGGAAAAACAAC 174
QY 151 GATCTGTCCATCTGCTAGAGATGTTTCAAGAGCGCTGTGTCATTTCTCCCTGGCAGCA 210
DB 175 GATCTGTCCATCTGCTAGAGATGTTTCAAGAGCGCTGTGTCATTTCTCCCTGGCAGCA 234
QY 211 CAACCTGTGCAAGAAATGTGCAAGTACATCTTCCAGGCTCTTAACCGTAATTACCCAC 270
DB 235 CAACCTGTGCAAGAAATGTGCAAGTACATCTTCCAGGCTCTTAACCGTAATTACCCAC 294
QY 271 AAGGAGAGGACCAACCGTGAGATCAAGGGGGCGCTTCGGCTGTCCCTCTGCAACATGA 330
DB 295 AAGGAGAGGACCAACCGTGAGATCAAGGGGGCGCTTCGGCTGTCCCTCTGCAACATGA 354
QY 331 GGTGTGTGTTAGACAGACATGGGGTCTATGACTGAGAGAGAACTGCTCGTGAAGAAAT 390
DB 355 GGTGTGTGTTAGACAGACATGGGGTCTATGACTGAGAGAGAACTGCTCGTGAAGAAAT 414
QY 391 TATTGATATCTTCAAGCAGAAATCCACGAGCCAGAAAAAAATTGACCAAGCCATGTG 450
DB 415 TATTGATATCTTCAAGCAGAAATCCACGAGCCAGAAAAAAATTGACCAAGCCATGTG 474
QY 451 TGAAGAGATGAAGAGAAACCATCAATCTATTGTCTGAACCTGTGAAGTCCCACTG 510
DB 475 TGAAGAGATGAAGAGAAACCATCAATCTATTGTCTGAACCTGTGAAGTCCCACTG 534
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RESULT 4
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mRNA sequence.
ACCESSION BG674823
VERSION BG674823.1 GI:13906219
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 790)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Straube, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LLM10594 row: f column: 15
High quality sequence stop: 776.
Location/Qualifiers

FEATURES

source

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1..790
/organism="Homo sapiens"
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/clone="IMAGE:4746254"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Skn3"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: oligo dT.  
Average insert size 1.5kb. Library constructed by Life  
Technologies. Note: this is a NCI_CGAP library."
```

ORIGIN

Query Match 21.8%; Score 565.2; DB 4; Length 790;
Best Local Similarity 84.3%; Pred. No. 1e-137;
Matches 666; Conservative 0; Mismatches 108; Indels 16; Gaps 2;

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DB 1 CAGCAGGAATCCACCGGCGGCAAGAAAAAATTGACAGCCCATGTGTGAAGCATGA 60
QY 463 AGAGGAAGATGAACATCTATTGTCTGAACCTGGAAGTCCCACTGTTCTTTGCAA 522
DB 61 AGAGGAAGATGAACATCTATTGTCTGAACCTGGAAGTCCCACTGTTCTTTGCAA 120
QY 523 GGTTTTGGCGCCCATTAAGACTGCGAGTGGTCCCTGACTCATGTGTTCCAGAGCA 582
DB 121 GGTGTTTGGTGCACAAAGATGCGCAGTGGTCCCTGACTCATGTGTTCCAGAGCA 180
QY 583 GAAGTCAGACTCAAGTATGTTTGTCTGACTTGTGGAGCAAGATGATCCAGGG 642
DB 181 GAAGTCAGACTCAAGTATGTTTGTCTGACTTGTGGAGCAAGATGATCCAGGG 240
QY 643 TGTGATGAGCAGCTGAGGACACCTGTAAACATATTGAAGTGTGCGAAGACGAA 702
DB 241 AGTATATGAGCAGCTGAGGACACCTGTAAACATATTGAAGTGTGCGAAGACGAA 300
QY 703 ACAGGACCTGTGTAGAAATTTGATACCTTATACGGCATCTGAGAGAGAGAACTGA 762
DB 301 ACAGGACCTTTGTAGAAATTTGATACCTTATACGGCATTTTGAAGAGAGAAATGA 360
QY 763 AATGACCAAGCATCACTGGAACAAGAGAGAACTGGAACATGTCCGAATCTTAT 822
DB 361 AATGACCAAGCATTAACCCGAAACCCAGAGAGAGAACTGGAACATGTCCGTCTGAT 420
QY 823 CAGGAATATTTCGATACCTGAGGAACGTAATCAAGTTGTGGAAGCAGAAATCCAGTT 882
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QY 883 CATGATGAGCCCGAAATGCGAGATTTCTGCAAGATGCCAAGACCTGTTGCAAAAGAT 942
DB 481 TATGATGAGCGAAGAAATGCGAGTTTCTGCAAGATGCCAAGACCTGTTAAAAAAT 540
QY 943 CGTGAAGCATCAAGGCGTTTCAAGTGAAGAACTGAAGAGTTATGATCATGAG 1002
DB 541 CTCGGAAGCATCAAGGCAATTTCAAGTGAAGAAATGAACATGCGTATAGAAACATGAA 600
QY 1003 CAACCTCAGCTCAATGCAATGAGAGAAAGAAATTAATCCGGAATGACCTTTTAG 1062
DB 601 CCACTTCACTCACTCAATGAGAGAGAAAGATTAATGTAATTAATGCTTTTACG 660
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Oy		1063	AGAAGAGAAATGAGAAAGCA-----TGCGAGGAATATGATAAGAAAGAG	1109
Dd		661	AGAAATCATTAATGAGAAAGCAAGACGCCGAGAAAGAAAAAGAGAGAGAGAG	720
Oy		1110	AA---GGAGAGCATGCAGTACGTAGAACGAGCCAGAAAATGTTCAAATGACATCTTCAG	1166
Dd		721	AAGTGGAGAGAGAAAGCAGTACGTAGAAAGGTGAGAAATGTTCAAACAGAGTTCCAG	780
Oy		1167	GGGAAAGAGCA	1176
Dd		781	GAGAGCATGA	790
RESULT 5				
CK599151				
LOCUS				
DEFINITION		CK599151	826 bp mRNA linear EST 22-JAN-2004	
ACCESSION		AGNCOURT 17896510 NIH_MGC_234 Rattus norvegicus cDNA clone		
VERSION		IMAGE:7192411 5' , mRNA sequence.		
KEYWORDS		CK599151		
SOURCE		EST.		
ORGANISM		Rattus norvegicus (Norway rat)		
REFERENCE		Rattus norvegicus		
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
JOURNAL		Rattus.		
COMMENT		1 (bases 1 to 826) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics / NIH National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-rc@mail.nih.gov Tissue Procurement: Howard Jacobs cDNA Library Preparation: Express Genomics cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: LHAM1505 row: a column: 17 High quality sequence stop: 621. Location/Qualifiers 1..826 /organism="Rattus norvegicus" /mol_type="mRNA" /db_xref="taxon:10116" /clone="IMAGE:7192411" /tissue_type="heart, pooled" /lab_host="DH10B Tona" /clone_id="NIH_MGC_234" /note="Organ: heart; Vector: pExpress-1; Site 1: EcoRV, Site 2: NotI; RNA obtained from pooled heart tissue from a mix of male and female animals at 8 wk old. Tissues were snap-frozen and kept at -80C for two days before RNA extraction and purification (TRI-reagent method). cDNA was primed using Oligo-dT primer: 5'-GAGACTGCTTAGATCCGAGCGCCGCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size selection >1.4kb resulted in an average insert size of 2.2 kb. This primary library is normalized (non-normalized primary library is NIH_MGC_233) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library."		
FEATURES				
Source				
ORIGIN				
Query Match		20.4%	Score 529.6; DB 7; Length 826;	
Best Local Similarity		93.3%	Pred. No. 2,8e-128;	
Matches		599; Conservative	0; Mismatches 34; Indels 9; Gaps 4;	
Oy		11	ACCCTTACAGAGCTGTTGGGAGCACCTTTCCTTGCGACGACACTCAGGAGCAGGAGC	70

Db	65	ACACTTCGAGAAAGCCGTTCCGGAGACACCCCTTCCCTGCGGACACACC-----CAGGAC	118
QY	71	GGCAAGAAATAGACACTTCTCTGAATTTACAAAGCTCTTTCTTCCAAAGACAGACCATG	130
Db	119	GGCTTAGGAATATGACACTTCTCTGAATTTACAAAGCTTTCTTCCAAAGACAGACCATG	178
QY	131	GATTAACCTTGGAAAAAGCAACTGATCTGTCCCTACCTTGGCTTAAGATGTTTACGAACCTGTG	190
Db	179	GATTAACCTTGGAAAAAGCAACTGATCTGTCCCTACCTTGGCTTAAGATGTTTACGAACCTGTG	238
QY	191	GTCAATTCCTCCCTGCGACACCAACTCTGGACGAAAAATGTGCAGTGAATCTTCCAGAGCC	250
Db	239	GTCAATTCCTCCCTGCGACACCAACTCTGGACGAAAAATGTGCAGTGAATCTTCCAGAGCC	298
QY	251	TCTAACCCTGATCTTACCCACCAAGAGAGAGACACACCGTGGCATGACGGGAGCCGCTTCCG	310
Db	299	TCTAACCCTGATCTTACCCACCAAGAGAGAGACACACCGTGGCATGACGGGAGCCGCTTCCG	358
Db	311	TGTCCCTCTCTGACAGCATGAGTGTGTGTAGACAGACATGGGGTCTTATGATGACAGAG	370
QY	359	TGCCCTCTTGTGACAGCATGAAAGTGTGTGTAGACAGCATGGGGTCTTATGATGACAGAG	418
Db	371	AACTGCTCTCGTGGAAAAATATATTGATATCTTACAGAGAAATCCACAGGCCGAAAAA	430
QY	419	AACTGCTCTCGTGGAAAAATATATTGATATCTTACAGAGAAATCCACAGGCCGAAAAA	478
Db	431	AAATTTGACACGACCATATGTGTGAAGACATGAAAGAGAAACGATCAATCTTATGTCTG	490
QY	479	AAATTTGACACGACCATATGTGTGAAGACATGAAAGAGAAACGATCAATCTTATGTCTG	538
Db	491	AACTGTGAAGTGCCACCTCTTCTTGTGACAGGTTTTTGGCGCCATTAAGAGCTGCCAG	550
QY	539	AACTGTGAAGTGCCACCTCTTCTTGTGACAGGTTTTTGGCGCCATTAAGAGCTGCCAG	598
Db	551	GTGGCTCCCCCTGATCTCATGTGTTTCCAGAGCAGAAATGCAAGCTCATGTATGTATGTCT	610
QY	599	GTGGCTCCCCCTGATCTCATGTGTTTCCAGAGCAGAAATGCAAGCTCATGTATGTATGTCT	657
Db	611	GTACTTGTGGAGCAACGATAGGTGCAGGGTGTGATCAGC	652
QY	658	GTACTTGTGGAGAC-ACGACACAGT-CAGGGTGTGATCAGC	697
Db	658	GTACTTGTGGAGAC-ACGACACAGT-CAGGGTGTGATCAGC	697

Email: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
 Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
 and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
 Sugahara, Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Akawa, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, I.,
 Alkawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
 Hayashizaki, Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.
 e mouse tissues.

FEATURES

source
 Location/Qualifiers
 1..672
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="DB30041C10"
 /tissue_type="heart"
 /dev_stage="16 days neonate"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 16 days neonate
 heart"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGCGGCCGCCACCTCGAGTTTCTTTTCTTTTNN 3']. cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence [5'
 GAGAGAGAGTTCTGAGTAAATTAAATTAATCCCCCCCCCC 3']. cDNA
 was cleaved with BamHI and XhoI. Vector: a modified
 Bluescript KS(+) after bulk excision from Lambda FLX I."

ORIGIN

Query Match 20.1%; Score 521.4; DB 2; Length 672;
 Best Local Similarity 98.2%; Pred. No. 3.8e-126;
 Matches 558; Conservative 0; Mismatches 7; Indels 3; Gaps 3;
 Oy | CCTTACGAGAGCTTTCGGGAGACCTTCCCTTGGAGACACTGAGGAGGAGCG 71
 Db | CCTTACGAGAGCTTTCGGGAGACCTTCCCTTGGAGACACTGAGGAGGAGCG 142
 Oy | 72 GCAGGAAATGAGCACTTCTGGAATTAAGAATCTTTCTCCAAAGAGGAGCAATAG 131
 Db | 143 GCAAGGAATGAGCACTTCTGGAATTAAGAATCTTTCTCCAAAGAGGAGCAATAG 202
 Oy | 132 ATTAATTGGAAGAAAGAACTGATCTGCCATCTGCTTGAAGATGTTCAAGAGCTGTGG 191
 Db | 203 ATTAATTGGAAGAAAGAACTGATCTGCCATCTGCTTGAAGATGTTCAAGAGCTGTGG 262
 Oy | 192 TCATCTCCCTTGCAGAGCAACCTGTGAGGAAATGAGCAATGATCTTTCCAGGCGCT 251
 Db | 263 TCATCTCCCTTGCAGAGCAACCTGTGAGGAAATGAGCAATGATCTTTCCAGGCGCT 322

Oy | 252 CTAAACCCGTAATTACCAAGAGAGGAGGACCAACCGTGATCAGGGGGCGCTTCGCT 311
 Db | 323 CTAAACCCGTAATTACCAAGAGAGGAGGACCAACCGTGATCAGGGGGCGCTTCGCT 382
 Oy | 312 GTCCCTCTCTGACAGCATGAGTGGTGTGTAAACAGACATGGGGTCTATGACCTGACAGGA 371
 Db | 383 GTCCCTCTCTGACAGCATGAGTGGTGTGTAAACAGACATGGGGTCTATGACCTGACAGGA 442
 Oy | 372 ACCTGCTGTGAAAAAACAATTATGATATCTACAGCAGAAATCCACAGGCCAGAAAAA 431
 Db | 443 ACCTGCTGTGAAAAAACAATTATGATATCTACAGCAGAAATCCACAGGCCAGAAAAA 502
 Oy | 432 AATTGACACACCCATGTGAAAGAGCATGAAAGAACCCATCAACATCTATTGTCTGA 491
 Db | 503 AATTGACACACCCATGTGAAAGAGCATGAAAGAACCCATCAACATCTATTGTCTGA 562
 Oy | 492 ACTGTGAAGTGGCCACCTGTCTTGTGCAAGGTTTGGCGCCATAGAGACTGCCAGG 551
 Db | 563 ACTGTGAAGTGG-CCACCTGTCTTGTGCAAGGTTTGGCGCC-TTAAAGACTGCCAGG 620
 Oy | 552 TGGCTCCCTGATCATGTGTTCCAGAG 579
 Db | 621 TGGCTCCCTC-GACTCATGTGTTCAAGAG 647

RESULT 7
 LOCUS CV026849 647 bp mRNA linear EST 20-AUG-2004
 DEFINITION 4912 Full length cDNA from the Mammalian Gene Collection Homo
 sapiens cDNA 5' similar to BC007750, mRNA sequence.
 ACCESSION CV026849
 VERSION CV026849.1 GI:51484871
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Rual, J.F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S.,
 Dricot, A., Li, N., Rosenbery, J., Lamesch, P., Vidalain, P.O.,
 Clingingsmith, R.R., Hartley, J.L., Espósito, D., Cheo, D., Moore, T.,
 Simmons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C.,
 Vandenhaute, J., Guisick, M.E., Albala, J.S., Hill, D.E. and Vidal, M.
 Human ORFome Version 1.1: a Platform for Reverse Proteomics
 Genome Res. (2004) In press
 CONTACT: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739
 Email: Marc.Vidal@dfci.harvard.edu

ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
 results from a PCR reaction using an MGC Full-length cDNA as
 template DNA and ORF specific primers
 PCR Primers
 FORWARD: ATGAGCGCATCTGGAATTAC
 BACKWARD: CATTCAATTAGGAGAGTTCAACA
 Insert Length: 647 Std Error: 38.00
 Plate: 11063 row: 01 column: H
 Seq primer: ACTGGCCGTGCTTTTACAACTGCTGCTGATCTGGGAAAC
 High quality sequence start: 101
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 POLYA=NO.

FEATURES

source
 Location/Qualifiers
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 /tissue_type="mixed"
 /clone_lib="Full Length cDNA from the Mammalian Gene
 Collection"

/note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 Donor vector. Reference: MGC (Mammalian Gene Collection) Program Team. Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"

ORIGIN

Query Match 19.6%; Score 508.2; DB 7; Length 647;
Best Local Similarity 89.0%; Pred. No. 1.2e-122;
Matches 549; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 80 ATGAGCACTCTCTGCAATTCAGTCTTCTCCAAAGAGCAGACCATGATTAATTG 139
DB 1 ATGAGCCCACTCTGCAATTCAGTCTTCTCCAAAGAGCAGACCATGATTAATTG 60
QY 140 GAAAGCACTGATCTGCTCCATCTGCTTGAAGATGTTCAAGAGCCTGTGCTATTCTC 199
DB 61 GAGAGCACTGATCTGCTCCATCTGCTTGAAGATGTTCAAGAGCCTGTGCTATTCTC 120
QY 200 CTTTGCAGACCAACCTGTGAGAAATGTGCCAGTACATCTTCCAGGCTCTTAACCCG 259
DB 121 CTTTGCAGACCAACCTGTGAGAAATGTGCCAGTATTTTCCAGGCTCTTAACCCG 180
QY 260 TACTTACCAACAAGAGGAGCACCAGCTGAGCATCAGGGGCGCTTCGCTGCTCCCTCC 319
DB 181 TATTTGCCCAAGAGAGGAGTACCAAGCATCAGGGGCGGATTCCTGCTCCCTCCCTCC 240
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DB 241 TGTAAGCATGAGTGTGTTAGATGACATGAGGCTCTTACTGACAGAGAACTGCTC 300
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DB 361 CAGCCCACTGCTGAGAGCATGAGAGAGAGCATCAACTTATTTCTGAACTGAGAA 420
QY 500 GTGCCCACTGCTTCTGCTGCAAGGTTTGTGCGCCCATTAAGAGCTCCAGTGGCTCCC 559
DB 421 GTACCCCACTGCTTCTGCTGCAAGGTTTGTGCGCCCATTAAGAGCTCCAGTGGCTCCC 480
QY 560 CTGACTCATGTGTTCCAGAGCAGAGATCAGAGCTCAGTGTGTTGCTGTTGCTG 619
DB 481 CTGACTCATGTGTTCCAGAGCAGAGATCAGAGCTCAGTGTGTTGCTGTTGCTG 540
QY 620 GGAAGCAAGATGAGTCCAGGGGTGATGAGCCAGCTGAGAGCACTGTAAACATAT 679
DB 541 GGCAGCAAGATGAGTCCAGGGGTGATGAGCCAGCTGAGAGCACTGTAAACATAT 600
QY 680 GAGAGTGTGAGAAA 696
DB 601 GAGGAAATGTTGAGAAA 617

RESULT 8
CR754151 657 bp mRNA linear EST 02-SEP-2004
LOCUS CR754151 Rattus norvegicus muscle Sprague-Dawley Rattus norvegicus
DEFINITION CDNA clone GP0AA11ZD06, mRNA sequence.
ACCESSION CR754151
VERSION CR754151.1 GI:51866108
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 657)
AUTHORS Cros N., Tkatchenko A.V., Plesani D.F., Leclerc L., Leger J.J.,

TITLE Marini J.F. and Dechesne C.A.
JOURNAL Analysis of altered gene expression in rat soleus muscle atrophied by disuse
MEDLINE J Cell Biochem. 83 (3), 508-519 (2001)
PUBMED 21479502
11596118

COMMENT

Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
Genoscope sequence ID: GP0AA11ZD06Cp1.
Location/Qualifiers

FEATURES

source

1..657
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/mol_type="mRNA"
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/db_xref="taxon:10116"
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ORIGIN

Query Match 19.1%; Score 494.6; DB 7; Length 657;
Best Local Similarity 89.9%; Pred. No. 4.6e-119;
Matches 603; Conservative 0; Mismatches 49; Indels 19; Gaps 6;

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DB 1 TCTGAACCTTCAGGCCCTTCAGAGCGGAAACTGCGGATCCCTGTTTAACTTACTG 60
QY 1406 TATTAAGGCCAAAGCCGAGAAACAGCTCCAACTTGAATCTGATGGAGTGAAGT 1465
DB 61 TATTAAGGCCAAAGCCGAGAAACAGCTCCAACTTGAATCTGATGGAGTGAAGT 120
QY 1466 CTGGGTCAATAAGGGCTCTGGGATTTGAGATTCAGTGTGCACTCCGAGAACTGCA 1525
DB 121 CTGAGTCAATAAGGGCTCTGGGATTTGAGATTCAGTGTGCACTCCGAGAACTGCA 180
QY 1526 GAAAGCCGCAACATGAGCAGCAGATGATGTTAAGAGTCTAAGTTCACTGACCT 1585
DB 181 GAAAGCCGCAACATGAGCAGCAGATGATGTTAAGAGTCTAAGTTCACTGACCT 240
QY 1586 ACCTTCAGATTTGAGATTTGAGGCCCTTCTCCCAAGGACAGTCTCAGCTTGGGAGT 1645
DB 241 ACCTTCAGATTTGAGATTTGAGGCCCTTCTCCCAAGGACAGTCTCAGCTTGGGAGT 300
QY 1646 GGGGTTGGGG-TGATCTGAGCAGCTCCCAAGTCTTCTCTCTCTGTTGAAATTC 1704
DB 301 GGGGTTGGGGCTGATTTGAGCCAGCTCCCAAGTCTTCTCTCTCTGTTGAAATTC 359
QY 1705 CCTTAATGAATATTTATTTATCTGTTGCTGCCCTGTGCTGCTGCTGAGAAAGCAT 1764
DB 360 CCTTAATGAATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 419
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Db 530 CTAATCTGTTGAGAAAATGATTATGCTCAGAACAAAATTAATCTGATGAA 589

Qy 1944 GAAACTGATCTTCGCAAAATCTTTCATTGTTGAGAGAACTTCTGAAAGTTGTAGG 2003

Db 590 GAAACTGATCTTATGCG-----TTTATTTGGTGAGAAACATTTCTGAAAGGTGTAGG 643

Qy 2004 TGTGTTGCATG 2014

Db 644 TGTGTTGCCTG 654

RESULT 9

BU131273 827 bp mRNA linear EST 25-NOV-2002

LOCUS 603116770F1 CSEBCHL21 Gallus gallus cdna clone CHEST72k17 5', mRNA

DEFINITION

sequence.

ACCESSION BU131273 GI:25343198

VERSION BU131273.1

KEYWORDS

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

REFERENCE

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 827)

Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

2235534

12445392

COMMENT

Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 0161208930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

1. 827

/organism="Gallus gallus"

/mol_type="mRNA"

/strain="White Leghorn, Hisex"

/db_xref="taxon:9031"

/clone="CHEST72k17"

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ORIGIN

Query Match 18.7%; Score 483.4; DB 5; Length 827;

Best Local Similarity 77.2%; Fred. No. 4.6e-116;

Matches 626; Conservative 0; Mismatches 181; Indels 4; Gaps 3;

Qy 186 CTGTGTCATCTTCCTTCGAGCAGCACTGTGAGAAATGTGTCAGTGCATCTTCC 245

Db 3 CGGTGTCATCTTCCTTCGAGCAGCACTGTGAGAAATGTGTCAGTGCATCTTCC 62

Qy 246 AGGCTCTTAACCCGTACTTACCCACAGAGAGGCAACACCGTGGCATCAGGGGGCCGCT 305

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LOCUS 603118735F1 CSEBCHL21 Gallus gallus cdna clone CHEST7769 5', mRNA

DEFINITION

sequence.

ACCESSION BU129677

VERSION BU129677.1 GI:25341494

KEYWORDS

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Phasianidae; Gallus.

REFERENCE

1 (bases 1 to 927)

Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

2235534

GenCore version 5.1.6
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	1261	48.7	2098	9	HS4243489	Homo sapi
6	1131.6	43.7	1960	9	HS431704	Homo sapi
7	974.4	37.6	227536	2	AC141209	Mus muscu
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16	678.2	26.2	172684	10	AC138605	Mus muscu
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ALIGNMENTS

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DEFINITION Sequence 3 from Patent WO0206318.
ACCESSION AX418850
VERSION AX418850.1 GI:21523714
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE Olson, E.N. and Spencer, J.A.

AUTHORS
TITLE Methods and compositions for stabilizing microtubules and intermediate filaments in striated muscle cells

JOURNAL Patent: WO 0206318-A 3 24-JAN-2002;

BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)

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ORIGIN

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 REFERENCE
 AUTHORS
 1 Isegai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
 Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
 Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
 Masuko,Y.
 TITLE
 JOURNAL
 Full-length cDNA sequences
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 Db 513 GCGAGGTGCTCCCTGACCTCATGTGTTTCAAGAGAGAAAGTCAAGACTCATGATGATA 572
 Qy 606 TTGCTGATCTTGTGAGAGACAGATAGATTCAGGGTGTGATCAGCAGCTGGAGACA 665
 Db 573 TGGCAGATCTCTGTGGAGAGACAGATGATGATCCAGGGAGTATCAGCAGCTGGAGACA 632
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 Db 633 CCGTGAATACTATTGAGAGAGTGTGTGCAAGAAACAGAAACAGACTGTGTGAGAAATTG 692
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 KEYWORDS oligo capping; fls (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Oca,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R.,
 Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
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 Kikawa,E., Omura,Y., Ade,K., Kamihara,K., Katsuta,N., Sato,K.,
 Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H.,
 Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M.,

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RESULT 5
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 DEFINITION AJ243489.1 GI:14588847
 ACCESSION alternative splicing; MURF2; RING finger protein 29; RNF29 gene;
 VERSION signal transduction; titin zinc-finger anchoring protein; tizian.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Iakovenko, A. and Gautel, M.
 TITLE Titin-associated zinc-finger proteins link titin kinase to
 JOURNAL transcriptional control
 REFERENCE U. Muscle Res. Cell Motil. 21, 833-833 (2000)
 AUTHORS 2
 TITLE Pizon, V., Iakovenko, A., Van Der Ven, P. F., Kelly, R., Fatu, C.,
 FIRST, D. O., Karsenti, E., and Gautel, M.
 JOURNAL Transient association of titin and myosin with microtubules in
 MEDLINE nascent myofibrils directed by the MURF2 RING-finger protein
 PUBMED J. Cell. Sci. 115 (Pt 23), 4469-4482 (2002)
 REFERENCE 3 (bases 1 to 2098)
 AUTHORS Gautel, M. S.
 TITLE Direct Submission

JOURNAL Submitted (29-JUN-1999) Gautel M.S., Physikalische Biochemie,
 Max-Planck-Institut fuer molekulare Physiologie, Otto-Hahn-Strasse
 11, Dortmund, 44227, GERMANY
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ORIGIN
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 Best Local Similarity 82.0%; Pred. No. 2,6e-308;
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 DB 573 AAAAAAATTTGACAGCCCATGTGTGAAGAGATGAAGAGAACCATCAATCATATT 632
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Oy	606	TTGCTGTACTGTGGGAAGCAACGATAGAGTCCAGAGGTGTATCAGCCAGCTGAGAGCA	665
Db	753	TGCGCATCTCGTGGGAGCAACGATCAGTCCAGGGAGTATCAGCCAGCTGGAAGACA	812
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Oy	726	ATCACTATACGGGATCCTGGAGAGAGAAAGACTGAATATACCAAGCCATCACTCGAA	785
Db	873	ATTACGTGTATGGCATTTTGGAGAGAGGAAGATGAATACCAAGCATCTTACCGGAA	932
Oy	786	CACAGAGAGAGAACTGGAACATGTCGAACTTTATCAGAAAGTATTTCCATCACTGG	845
Db	933	CCCAAGAGAGAAACTGGACATGTCCCTGTCTGTATCAAAAAGTATTCATCATATTGG	992
Oy	846	AGAACGATCAAGTGTGGTGGAGTCCAGAAATCCAGTTATAGATGAGCCGAAATGGCAG	905
Db	993	AGAACGTCCTCAAAAGTTGGTGTAGTCCAGAAATTCAGTTTATGAGATGACCAAAATGGCAG	1052
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Db	1407	CCTCTCCAGAGCCACTTCAGAGCCCTGCCAACCCTGCGGGAAGCCCCGTGTACACAGGGGG	1466
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Oy	1491	TTAGAGATTCCAGTGTGACGTCCGCAAGTGGCAGAAAGCCGCAACCAATGACAGGAG	1550
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OY	1611	CTTCTCCCAAGGACACCTTCGACACCTTGGGAAATGGGGGCG--GGGATCTCAAGCAG	1659
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OY	1730	TTGCTGCCCC-CTGTCTGCTGTGCTGAAAGCATATGCGAGCGAGAAACAGTGGAAAT	1788
Db	1886	CTGCTGCCCCCTGTGCTGCTGTGCTGAGATGTCATGTGGCAGCAGAGCCCAAGTGAA	1945
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Db	2050	ATATTTTGAAGAAATGATGTGCAGAAACACTCGAAATATATTAATCTTGAAT	2098

RESULT 6	
LOCUS	HSA431704
DEFINITION	HSA431704 1960 bp mRNA linear PRI 08-NOV-2002
ACCESSION	Homo sapiens RNF29 gene for RING finger protein 29, alternative C-terminal isoform.
VERSION	AJ431704
KEYWORDS	AJ431704.1 GI:24939888 alternative splicing; MURF2; RING finger protein 29; RNF29 gene; signal transduction; titin zinc-finger anchoring protein; tizian. Homo sapiens (human)
SOURCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 Iakovenko,A. and Gautel,M. Titin-associated zinc-finger proteins link titin kinase to transcriptional control
AUTHORS	J. Muscle Res. Cell Motil. 21, 833-833 (2000)
JOURNAL	2
REFERENCE	Picton,V., Iakovenko,A., Van Der Ven,P.F., Kelly,R., Fatu,C., Purst,D.O., Karsenti,E. and Gautel,M. Transient association of titin and myosin with microtubules in nascent myofibrils directed by the MURF2 RING-finger protein
AUTHORS	J. Cell. Sci. 115 (Pt 23), 4469-4482 (2002)
JOURNAL	MEDLINE 12414993 PUBMED 12414993
REFERENCE	3 (bases 1 to 1960) Gautel,M.S.
TITLE	Direct Submission
JOURNAL	Submitted (21-FEB-2002) Gautel M.S., Physikalische Biochemie, Max-Planck-Institut fuer molekulare Physiologie, Otto-Hahn-Strasse 11, Dortmund, 44227, GERMANY
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Query Match 43.7%; Score 1131.6; DB 9; Length 1960;
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 DB 333 CTGTGTCATCTTCTTCCGACAGCAACTGTGTCAGAAATGTCAGTGAATCTTC 392
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 QY 1026 GAGAGAGAAATTTATCTCGTAAATTTGACTTTTCTAGAGAGAGAGAGAGAGAGATG 1085
 DB 1173 GAGAGAGAAATTTATCTCGTAAATTTGACTTTTCTAGAGAGAGAGATGAGAGAGAG 1232
 QY 1086 CAGAG-----AATGATGAGAGAGAGAGAGAGAGAGATGAGAGAG 1130
 DB 1233 AAGAGGCGAG 1292
 QY 1131 TAGAAGGCGAG 1190
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 QY 1191 CTGACAGGCTCTGACAGTCTCCGAGAGCTTCAGGTGCGCCAGAGCACTACTGCTT 1250
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 DB 1587 CCAACCAACCACTTGTGATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1646
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 QY 1551 CAGTGAAGTGTGAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1594
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RESULT 7
 AC141209 22736 bp DNA linear HTG 01-OCT-2004
 LOCUS Mus musculus chromosome 3 clone Rp23-199MS map 3, *** SEQUENCING IN
 DEFINITION PROGRESS ***, 6 unordered pieces.
 ACCESSION AC141209
 VERSION AC141209.7 GI:52694746
 KEYWORDS HTG; HTGS PHASE1; HTGS_FULFILLTOP; HTGS_ACTIVEFIN.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCES
 1. Bliren,B., Nusbäum,C. and Lander,E.
 1. (bases 1 to 227536)
 TITLE Mus musculus chromosome 3, clone Rp23-199MS
 JOURNAL Unpublished
 2 (bases 1 to 227536)

AUTHORS

Birtten, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Deatrelano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, C., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Menes, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Pihunkha, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

REFERENCE

AUTHORS

Submitted (10-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 227536)
 Birtten, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Deatrelano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Menes, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Pihunkha, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

Submitted (01-OCT-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Sep 27, 2004 this sequence version replaced gi:52694042.
 All repeats were identified using RepeatMasker:
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/MIT Center for Genome Research

Center code: WIRK

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@road.mit.edu

Project Information

Center project name: L19666

Center clone name: 199_M_5

* NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 7177: contig of 7177 bp in length
 * 7178 7277: gap of unknown length
 * 7278 21433: contig of 14156 bp in length
 * 21434 21533: gap of unknown length

FEATURES		source
* 21534 40262: contig of 18729 bp in length		
* 40263 40362: gap of unknown length		
* 40363 92478: contig of 52116 bp in length		
* 92479 92578: gap of unknown length		
* 92579 187577: contig of 94999 bp in length		
* 187578 187677: gap of unknown length		
* 187678 227536: contig of 39859 bp in length.		
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Best Local Similarity		98.2%; Pred. No. 2e-235;
Matches 1006; Conservative 0; Mismatches 16; Indels 2; Gaps 2;		
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Qy	1628	TCGACAGCTTGGGAGATGGGAGTGAGG- TGATCTTGAAGCAGCTGCACAGCTTCTCC 1686
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Qy	1687	TTCTCTGTTTGAATTCCTTAATGAATATTTATTTCTGTTGCTGCCCCCTGTCTG 1746
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Qy	1807	AGGGACCTCTGACAGAGATTTCTGAAAGCAAAACAAATCAACACACACACCTT 1866
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Qy	1867	TAATTCAGATGACTTATCTCACTCATTTGAGAAATGATTTATGCTGAGAACAAATTTACA 1926
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Qy	1927	GAATAATCTCTTCTGAAAGAACTTGATCTCTGCAAACTTTATATTTGTTGAAACCT 1986
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Qy	1987	TCGAAAGTTGTGATGAGTGTGATGATGCTGTGTATCAGCCATAAGTGCAAGTGATTA 2046
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Qy	2047	CAAAAGTGCAAGACACTCTCCAGCCTCCCTCAGGCTTCTGTTATTTTGAACGCTTGT 2106
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Qy	2287	CACACGTCATGTCGAGAGGCAAAATCTTAGGCACTCTTTTGAATTTTCTTAC 2346
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 DB 133228 GGAGCTGTCATCTTCTTAAGTGTCTGCAGATAGCAGCAATCTGATTAATCTGTGAGCAA 133287
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 DB 133348 TCCCCCTCTCTCCCTGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 133407
 QY 2587 CTCC 2590
 DB 133408 CTCC 133411

RESULT 8
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 LOCUS Homo sapiens ring finger protein 29, transcript variant 3, mRNA
 DEFINITION (CDNA clone MGC:12836 IMAGE:4110783), complete cds.
 ACCESSION BC007750
 VERSION BC007750.2 GI:33871581
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1741)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klapper, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.E., Brownstein, M.J., Ushed, T.B., Tomshyuk, L., Stachurski, P., Prange, C., Raha, S.S., Loughellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hu, X., Gibbs, R.A., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butler, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Scheraga, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 JOURNAL 12477932
 PUBMED 2 (bases 1 to 1741)
 REFERENCE Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (11-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK NH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT On Aug 19, 2003 this sequence version replaced gi:14043531.
 Contact: MGC help desk
 Email: gcgaps-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),

Gatherburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nci.nih.gov
 Akhtar, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granice, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Khong, P., Latic, P., Legaspi, R., Maduro, O.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantrop, S., Thomas, P.J., Touchman, J.W., Tsurgem, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Whigins, L., Young, A., Zhang, L.-H. and Green, E.D.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/INL ac: <http://image.lnl.gov>
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 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14916468.
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 DB 299 AGGCTCTTAACCTGCTTAACTTAAACCAAGAGAGGAGTACCAACGATGATGAGGGGCGAT 358
 QY 306 TCCGCTGTCTCTCTCTCAAGATGAGTGTGTTAAGACAGACATGGGCTTATGATGCTGC 365

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Db 419 AGAGAACTCTCGTGGAAAAATATCATTTGACATCTACAGCAGAAATCCACGAGCCAG 478
Qy 426 AAAAAAATTTGACCAAGCCCATGTGTGAAGCATGAAGAGAAAGCATCAACATCTATT 485
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RESULT 9
AX746908 2634 bp mRNA linear PAT 20-JUN-2003
LOCUS AX746908
DEFINITION Sequence 433 from Patent EP1308459.
ACCESSION AX746908
VERSION AX746908.1 GI:32131296

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
location/Qualifiers
ORIGIN
Query Match 35.2%; Score 910.8; DB 6; Length 2634;
Best Local Similarity 84.2%; Pred. No. 1.6e-219;
Matches 1056; Conservative 0; Mismatches 177; Indels 21; Gaps 2;
Qy 66 GGGAGCGAAGAGAAATGAGCACTTCTGTAATTACAAATCTTTCTCAAGAGCAGCAGA 125
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RESULT 10
 AK091310 2634 bp mRNA linear PRI 30-JAN-2004
 LOCUS
 DEFINITION Homo sapiens cDNA FLJ33991 fis, clone DFNES2007332, moderately
 similar to Mus musculus RING-finger protein MURF mRNA.
 AK091310
 ACCESSION AK091310.1 GI:21749650
 VERSION
 KEYWORDS oligo capping; fis (full insert sequence).
 SOURCE
 ORGANISM Homo sapiens
 Homo sapiens
 Mammalia; Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS
 1 Oca,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R.,
 Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Mafile,H.,
 Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
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 Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamaeishi,H.,
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JOURNAL
 PUBLISHED
 REFERENCE
 AUTHORS
 Tashiro,H., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S.,
 Fukuzumi,Y., Fujimori,Y., Komiyama,M., Sugiyama,T., Irie,R.,
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 Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
 Nagahara,K., Masuo,Y., Nagai,K. and Isogai,T.
 NEDO human cDNA sequencing project
 Unpublished
 3 (bases 1 to 2634)
 Isogai,T. and Yamamoto,J.
 Direct Submission
 Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@ri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction: Helix Research Institute (HRI) (supported by Japan
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
 HRI, and Biotechnology Center, National Institute of Technology and
 Evaluation; clone selection for full insert sequencing: HRI and
 RAB; annotation: HRI and RAB.
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 dermal fibroblasts"
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Qy 606 TTGCTGTACTTGTGGGAAAGCAAGATAGAGTCCAGGGTGTGATCAGCCAGCTGAGAGCA 665
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Qy 666 CCTGTAAAACTATTGAGAGTGTGTGCAAGAAAGCAAGAAACAGAGCTGTGTGAAATTTG 725
Db 963 CCTGTAAAACTATTGAGAGTGTGTGCAAGAAAGCAAGAAACAGAGCTGTGTGAAATTTG 1022
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Qy 1191 CTGAG 1250
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Db 1557 CCTCTCAG 1612

RESULT 11
LOCUS HSA243488 1810 bp mRNA linear PRI 08-NOV-2002
DEFINITION Homo sapiens RNF29 gene for RING finger protein 29, 50kDa isoform.
ACCESSION AJ243488
VERSION AJ243488.1 GI:14588845
KEYWORDS alternative splicing; MURF2; RING finger protein 29; RNF29 gene; signal transduction; titin zinc-finger anchoring protein; tizian.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Iakovenko, A. and Gautel, M.
TITLE Titin-associated zinc-finger proteins link titin kinase to transcriptional control
JOURNAL U. Muscle Res. Cell Motil. 21, 833-833 (2000)
REFERENCE Pizon, V., Iakovenko, A., Van Der Ven, P. F., Kelly, R., Fatu, C., Furst, D. O., Karsenti, E. and Gautel, M.
AUTHORS Transient association of titin and myosin with microtubules in nascent myofibrils directed by the MURF2 RING-finger protein
JOURNAL J. Cell. Sci. 115 (Pt 23), 4469-4482 (2002)
MEDLINE 22302063
PUBMED 12414993
REFERENCE 3 (bases 1 to 1810)
AUTHORS Gautel, M. S.
JOURNAL Direct Submission
Submitted (29-JUN-1999) Gautel M. S., Physikalische Biochemie, Max-Planck-Institut fuer molekulare Physiologie, Otto-Hahn-Strasse 11, Dortmund, 44227, GERMANY
FEATURES
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Query Match 35.1%; Score 909.2; DB 9; Length 1810;
Best local similarity 84.2%; Pred. No. 4e-219;
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RESULT 12

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LOCUS      BT007212      1311 bp      mRNA      linear      PRI 13-MAY-2003
DEFINITION Homo sapiens ring finger protein 29 mRNA, complete cds.
ACCESSION  BT007212
VERSION     BT007212.1
KEYWORDS   FLI cDNA.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 1311)
AUTHORS   Kaulina,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
           Kaulina,N., Raphael,J., Morelra,D., Kelley,T., Labaer,J., Lin,Y.,
           Pheasant,M., and Farmer,A.
TITLE      Cloning of human full-length cDNAs in BD Creator(TM) System Donor
vector
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 1311)
AUTHORS   Kaulina,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
           Kaulina,N., Raphael,J., Morelra,D., Kelley,T., Labaer,J., Lin,Y.,
           Pheasant,M., and Farmer,A.
TITLE      Direct Submission
COMMENT     Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
           Circle, Palo Alto, CA 94303, USA
           This cDNA clone is a part of a collection of human full length
           expression clones generated by BD Biosciences Clontech and the
           Harvard Institute of Proteomics. Each cDNA has been cloned in two
           forms: with and without stop-codon (to allow fusion with C-terminal
           tag). The cDNA has been directionally cloned using BD in-fusion(TM)
           cloning system between the SalI and HindIII sites of the pDNR-DUAL
           vector. Additional sequences in the clone: 'ACC' after SalI site
           and before 'ATG' to provide Kozak consensus sequence; 'GG' after
           last codon and before HindIII site to maintain reading frame.
           Clone distribution: http://bioinfo.clontech.com/orfclones.
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Query Match      33.2%; Score 860; DB 9; Length 1311;
Best Local Similarity 84.0%; Pred. No. 1,1e-206;
Matches 1003; Conservative 0; Mismatches 170; Indels 21; Gaps 2;
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RESULT 13
BT008253

LOCUS BT008253 1311 bp mRNA linear SYN 13-MAY-2003
DEFINITION Synthetic construct Homo sapiens ring finger protein 29 mRNA,
partial cds.
ACCESSION BT008253
VERSION BT008253.1 GI:30585344
KEYWORDS FLI CDNA.
SOURCE synthetic construct
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1311)
AUTHORS Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Kundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,
Phelan,M., and Farmer,A.
TITLE Cloning of human full-length CDSs in BD Creator(TM) System Donor
vector
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1311)
AUTHORS Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Kundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,
Phelan,M., and Farmer,A.
COMMENT Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
Circle, Palo Alto, CA 94303, USA
This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD in-Fusion(TM)
cloning system between the SalI and HindIII sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'Acc' after SalI site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
last codon and before HindIII site to maintain reading frame.
Clone distribution: <http://bioinfo.clontech.com/orfclones>.
location/Qualifiers
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ACCESSION  CR354317
VERSION    CR354317.1 GI:45426612
KEYWORDS
SOURCE
ORGANISM   Gallus gallus (chicken)
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE
AUTHORS    Boardman,P.E., Bonfield,J.K., Brown,W.R.A., Carder,C., Chalk,S.E.,
            Croning,M.D.R., Davies,R.M., Francis,M.D., Grafham,D.V.,
            Hubbard,S.J., Humphray,S.J., Hunt,P.J., Maddison,M., McLaren,S.R.,
            Niblett,D., Overton,I.M., Rogers,J., Scott,C.E., Taylor,R.G.,
            Tickle,C. and Wilson,S.A.
TITLE      Direct Submission
JOURNAL    Submitted (09-MAR-2004) Sanger Institute, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: chickens@ms.umbst.ac.uk
COMMENT    BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
            sequencing project.
            This sequence is from the
            BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection,
            from a library constructed by Elizabeth Bosch. cDNA was prepared
            from RNA extracted from trunks,
            and poly A-tailed. BcORI-NotI cut cDNA was then ligated into the
            vector. Vector: pBluescript II KS(+); Site_1: BcORI; Site_2: NotI
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            Location/Qualifiers
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AC133956
VERSION AC133956.4 GI:38524721
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Belter, E., Bielicki, L., Elliott, G. and Haakenson, W.
TITLE The sequence of Mus musculus BAC clone RP23-347E10
JOURNAL Unpublished (2001)
AUTHORS Wilson, R.
REFERENCE
2 Wilson, R.
TITLE Sequencing of Mus musculus
JOURNAL Unpublished (2001)
REFERENCE
3 (bases 1 to 171261)

AUTHORS McPherson, J.D. and Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE
1 (bases 1 to 171261)
AUTHORS Wilson, R.K.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE
2 (bases 1 to 171261)
AUTHORS Wilson, R.K.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE
3 (bases 1 to 171261)
AUTHORS Wilson, R.
TITLE Direct Submission
JOURNAL Submitted (01-JAN-2004) Department of Genetics, Washington
University, 444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Nov 26, 2003 this sequence version replaced gi:35070665.
COMMENT
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@wustl.edu
----- Summary Statistics
Center Project name: M_BA0347E10

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
http://genome.wustl.edu

SOURCE INFORMATION:
The RPCI-23 BAC library has been constructed by Kazutoyo Osegawa
and Minako Tateo in the laboratory of Pieter de Jong
(http://www.chori.org) from female C57BL/6J mouse kidney and/or
brain genomic DNA. The clone and detailed information can be
obtained from Research Genetics, Inc. (http://www.resgen.com) or
Pieter de Jong and coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone. This clone is
overlapped by AC138605 and AC122837.

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GenCore version 5.1.6
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Run on: June 14, 2005, 20:19:07 ; Search time 443 Seconds
(without alignments)
9566.494 Million cell updates/sec

Title: US-10-775-627A-3

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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Patent No. 6740751					
GENERAL INFORMATION:					
APPLICANT: OLSON, ERIC					
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES					
FILE REFERENCE: MYOG:028US					
CURRENT APPLICATION NUMBER: US/09/908,988B					
PRIOR FILING DATE: 2000-07-18					
PRIOR APPLICATION NUMBER: 60/219,020					
NUMBER OF SEQ ID NOS: 6					
SOFTWARE: PatentIn Ver. 2.1					
SEQ ID NO 3					
LENGTH: 2590					
TYPE: DNA					
ORGANISM: Mus musculus					
FEATURE:					
NAME/KEY: CDS					
LOCATION: (80)..(1714)					
US-09-908-988B-3					
Query Match					
Best Local Similarity 100.0%; Score 2590; DB 4; Length 2590;					
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Qy 1081 AGATGACAGAGAAATAGATGAAGAGAGAGAGAGATGACATAGAAAGTGAAGAGAGC 1140
Db 1081 AGATGACAGAGAAATAGATGAAGAGAGAGAGAGATGACATAGAAAGTGAAGAGAGC 1140
Qy 1141 AGAAAAATGTTCAAAATAGCATCTTCAAGGGAGAGAGAGAGTCTGAGAAAAGCTGACAGCC 1200
Db 1141 AGAAAAATGTTCAAAATAGCATCTTCAAGGGAGAGAGAGAGTCTGAGAAAAGCTGACAGCC 1200
Qy 1201 CTCTCAGCTTCCCGCAGAGCTTCAAGGTGCCCCAGAGCATTAATCTGTTCTCTCAGA 1260
Db 1201 CTCTCAGCTTCCCGCAGAGCTTCAAGGTGCCCCAGAGCATTAATCTGTTCTCTCAGA 1260
Qy 1261 ACCGTTTTCATTCATGACACCTGCTGAGATGCTGTGTGACACAGGGGAGAGTGTGCC 1320
Db 1261 ACCGTTTTCATTCATGACACCTGCTGAGATGCTGTGTGACACAGGGGAGAGTGTGCC 1320
Qy 1321 CATTTGCTCTCAGAGACACACAGTCTGAAATTTCAAGCCCTTCAAGCAGGAGAACTGC 1380
Db 1321 CATTTGCTCTCAGAGACACACAGTCTGAAATTTCAAGCCCTTCAAGCAGGAGAACTGC 1380
Qy 1381 GGATCCCTGTGTTTAACCTAGTGTGTATTAAGGCCAAAGCCGAAAAACAGCTCAACCC 1440
Db 1381 GGATCCCTGTGTTTAACCTAGTGTGTATTAAGGCCAAAGCCGAAAAACAGCTCAACCC 1440

Db 1381 GGATCCCTGTGTTTAACCTAGTGTGTATTAAGGCCAAAGCCGAAAAACAGCTCAACCC 1440
Qy 1441 ACCTTGACATCATGGAGAGTGAAGGTCTGTGATCAAAATAGGCTCTGTGGCATGAGATTC 1500
Db 1441 ACCTTGACATCATGGAGAGTGAAGGTCTGTGATCAAAATAGGCTCTGTGGCATGAGATTC 1500
Qy 1501 CAGTGTGCACTCCGACAGAGAGTGCAGAGCCGCAACCAATGACAGGACAGTGAAGTGG 1560
Db 1501 CAGTGTGCACTCCGACAGAGAGTGCAGAGCCGCAACCAATGACAGGACAGTGAAGTGG 1560
Qy 1561 TAAGAGTCAAGTCAACCTGACAGTACCTCTGAGATTGGAATTTGAGGGCCCTTCTCCCA 1620
Db 1561 TAAGAGTCAAGTCAACCTGACAGTACCTCTGAGATTGGAATTTGAGGGCCCTTCTCCCA 1620
Qy 1621 GGAACAGTCTGACACCTTGGGGAGTGGGGGTGGGGTGAATCTGAGCAGCTGCCACGTC 1680
Db 1621 GGAACAGTCTGACACCTTGGGGAGTGGGGGTGGGGTGAATCTGAGCAGCTGCCACGTC 1680
Qy 1681 TTCTCTCTCTCTGTGTGAAATTCCTAAATGAATATTTATTTCTGTTGCTGCCCCC 1740
Db 1681 TTCTCTCTCTCTGTGTGAAATTCCTAAATGAATATTTATTTATTTCTGTTGCTGCCCCC 1740
Qy 1741 TGTCTGCTGTGGTGAAGACATAGGACAGAGAAACAGGTGGAAATTCACACGATTC 1800
Db 1741 TGTCTGCTGTGGTGAAGACATAGGACAGAGAAACAGGTGGAAATTCACACGATTC 1800
Qy 1801 ATATGAAGGGAGCCTCTGACACAGATTTCTGAAGAGCAAAACAAACATACACACC 1860
Db 1801 ATATGAAGGGAGCCTCTGACACAGATTTCTGAAGAGCAAAACAAACATACACACC 1860
Qy 1861 ACCCTTAAATTCAGATGACTTATCTCAGCTGAGAGAAATGATTAATGCTCAGAACAA 1920
Db 1861 ACCCTTAAATTCAGATGACTTATCTCAGCTGAGAGAAATGATTAATGCTCAGAACAA 1920
Qy 1921 ATTAACGAAAAATCTCTGTGAAGAACTTGAATCTTCTGCAATTTCTGATGAG 1980
Db 1921 ATTAACGAAAAATCTCTGTGAAGAACTTGAATCTTCTGCAATTTCTGATGAG 1980
Qy 1981 AAACCTTCTGAAGGTTGTGAGGTGTGTGATGATGCTGTGTATCAGCCATAGTGCACAG 2040
Db 1981 AAACCTTCTGAAGGTTGTGAGGTGTGTGATGATGCTGTGTATCAGCCATAGTGCACAG 2040
Qy 2041 TGGTAAACAAGTGCAGAACACTCTCCAGCCTCCCTCAGGCTTCTGTGATTTTAAAGAC 2100
Db 2041 TGGTAAACAAGTGCAGAACACTCTCCAGCCTCCCTCAGGCTTCTGTGATTTTAAAGAC 2100
Qy 2101 GCTTGTGCCCTTTGCTTTTCTCCTAGCAATTTGAGAGGTGAGAGTGAATGTTCAATGTCAGT 2160
Db 2101 GCTTGTGCCCTTTGCTTTTCTCCTAGCAATTTGAGAGGTGAGAGTGAATGTTCAATGTCAGT 2160
Qy 2161 TCCAACTGACCGATTTATCAAAATATGAGATTTGTCATCTGACCAAAAGCTATGAGGGC 2220
Db 2161 TCCAACTGACCGATTTATCAAAATATGAGATTTGTCATCTGACCAAAAGCTATGAGGGC 2220
Qy 2221 ACTGTAGAGGTTCTTTTCCCTATGATGTCATGGGTGCGCAGACAGGACTTTCCTTTACA 2280
Db 2221 ACTGTAGAGGTTCTTTTCCCTATGATGTCATGGGTGCGCAGACAGGACTTTCCTTTACA 2280
Qy 2281 TGTGGCCAGACGTTCATAGTCCAGAGGGCCAAAAATCTAGGGCAACCTTTTACANTTT 2340
Db 2281 TGTGGCCAGACGTTCATAGTCCAGAGGGCCAAAAATCTAGGGCAACCTTTTACANTTT 2340
Qy 2341 TCTAACCTTATTTATCATATCTCATTAATCATATCATATCATATCATATTTAATTTGAATTT 2400
Db 2341 TCTAACCTTATTTATCATATCTCATTAATCATATCATATCATATCATATTTAATTTGAATTT 2400
Qy 2401 CAAAGAGAGCTGTCTACTTTCTTAAAGTCTGTGCATAGCAGCAATCTGATATCTGTG 2460
Db 2401 CAAAGAGAGCTGTCTACTTTCTTAAAGTCTGTGCATAGCAGCAATCTGATATCTGTG 2460
Qy 2461 GAGCAACTGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2520
Db 2461 GAGCAACTGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2520

QY	2521	TTCTCTCCCCCTCTCCCTCTGCTCTCTCTCCCTCTGCTCTCCCTCTTCT	2580
Db	2521	TTCTCTCCCCCT	2580
QY	2581	TTCTCTCTCC 2590	
Db	2581	TTCTCTCTCC 2590	

Query Match	18.7%	Score 485.6	DB 3	Length 1757
Best Local Similarity	67.7%	Pred. No. 7.5e-128		
Matches 696	Conservative	0	Mismatches 329	Indels 3
				Gaps 1

Qy	112	CAAAAGACGAGACCATGAAATACCTTGAAAGAGACATGATCTGTCCATCTGGCTTGA	171
Db	148	CCAGGATGGGAAATCCCATGAGAACTTGGAGAGACGCTGATCTGCCATCTGCTGGA	207
Qy	172	GATGTTCCAGAACCTGTGTCTATTTCTCCCTTGCAGACCAACTGTGCAGAGAAATGTGC	231
Db	208	GATGTTTACCAAGCCAGTGTCTATCTTCCCGTGCAGACCAACTGTGCCGGAAGTGTGC	267
Qy	232	CAGTGACATCTTCCAGAGCCTCTAACCCGTACTTACCAAGAAGAGGACCAACCGTGGC	291
Db	268	CAATGATATTTTCCAGGCCCTTAAACCGATTTTGCACAAAGAGAGGTAACCACTATGGC	327
Qy	292	ATCAGGGGGCCGCTTCCGCTGTCCCTCTGCAGACATGAGGTGTGTTAGACAGACATGG	351
Db	328	ATCAGGGGGCCGATTCGCGCTGCCCATCTGTAGACATGAAGTGTTTTGATAGCATGG	387
Qy	352	GGTCTATGAGATCTGACAGAGAACTGTCTGTGTGAAAACATTTATGTAATCTTCAAGCAGA	411
Db	388	GGTATATGACTTCAAGAGAACTGTGTGTGAGAAACATCTCACTTCAAAACAGAA	447
Qy	412	ATCCACCA--GGCCAGAAAAAATTGGACAGAGCCCATGTGTGAAAGACATGAAGAGA	468
Db	448	GTGCTCCAGTGGGGCGCTGCAGAAAGGGCAGTCAACCCCATGTGCAAGAGACGAAGAATGA	507
Qy	468	ACGCATCAACATCTATTGTCTGAACTGTGAAGTGTCCACCTGTTCTTTGTGCAAGTTTY	528
Db	508	GAAATCAACATCTACTGTCTCACTGTGAGGTGCCACCTGTCTCAATGTGCAAGTGT	567
Qy	528	TGGCGCCCATTAAGACTGCGCAGAGTGGCTCCCTGTACTATGTGTTCCAGAGGCAGAAATGC	588
Db	568	TGGGATCCAAAGGCTCGCAGAGTGGCCCATTTGCAGAGTGTCTTCCAGGGGCAAAATAC	627
Qy	588	AGAGTCAAGTATGTTATGTCTGTACTTGTGTGGAAGCAACATAGATCTCAGAGTGTAT	648
Db	628	TGAATGAAATACTATATCTCATGCTGTGTGGCGGGGAATAGACCTGTGTGCAGAACCATAT	687

Oy	649	CAGCAGATGGAGGACACCTGTAAACATATGAGAGGTGCGAGAAAGCAGAAACAGGA	708
Dd	688	CACCTAGCTGAGGATTTCCGTCCAGTGCACAGAGAAACGTCACCGAGTAAAGAGAGA	747
Oy	709	CTGTGTGAGAAATTTGATCACTTAACGGCATCCTGGAGAGAGAAAGACTGAATGAC	768
Dd	748	GCTAGGCGAAGATTGACACGTTGTATGCCATCCTGGATGAGAAAGAAAGTAGATTGCT	807
Oy	769	CCAAAGCATCATCTGAAACACAGAGAGAGAACTGGAAACATGTCGAACTTTATCAGGA	828
Dd	808	GCACCGGATCCGACAGGACAGAGAGAAAGCTTAAGCTTCATCCAGGCGCCATCCAGCA	867
Oy	829	GTATTCGATACCTTGAGGAACGATATCCAAATTGTTGAGAGCAGAAATCCAGTTCATGGA	888
Dd	868	GTACACAGAGCAGGTGGCAAGTCCACAAAGCTGTTGAAATCTCCATCCAGTCCCTGGGA	927
Oy	889	TGAGCCCGAATGSCAGATATTTGCAAGATGGCAAGACCCGTGTGCAAAAGATCGTGA	948
Dd	928	CGAGCTTGGGGAGGCCACCTTCTCTTGACTGCCAAGCACTCATCAAAAGCATTTGTGA	987
Oy	949	AGCATCAAAGCGCTTTCAGATGAGAAACTAGAACAAAGTTATGAGATCATAGACCACTT	1008
Dd	988	AGCTTCCAGGCGCTGCAGCTGGGGAGAGACAGACAGGCGTTTGAACAATGCACTTCTT	1047
Oy	1009	CACGTGCATCTCAATAGAGAGAAATAATTCCTGTAATTTGACTTTTCTAGAGAGA	1068
Dd	1048	TACTTTGGATTTAAGCACATAGACAGCGCCCTGAGAGCCATTGACTTTGGGACAGATGA	1107
Oy	1069	GGAAGAGGAAGAAATGCAAGAGAAATAGATGAAGAGAGAGAAAGAGAGATGCAGTGA	1128
Dd	1108	GGAAGAGGAAGAAATTCATTGAAGAGAAAGATCAGAGAGAGAGAGATCCACAGAAAGGAA	1167
Oy	1129	AGTAGAG 1136	
Dd	1168	GGAAGAG 1175	

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RESULT 3
US-09-908-988B-1
; Sequence 1, Application US/09908988B
; Patent No. 6740751
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; TITLE OF INVENTION: IN STRLATED MUSCLE CELLS
; FILE REFERENCE: MT0G:028US
; CURRENT APPLICATION NUMBER: US/09/908,988B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1296)
; US-09-908-988B-1

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	Query Match	Similarity	Score	DB #	Length
	Best Local	63.8%	450.8	DB 4	1431
	Matches	702	Conservative	0	Mismatches 392; Indels 6; Gaps 1
QY	68	GACGGCAAGAAATAGACATCTTCTGAATTACAGCTTTCTCCAAAGACAGAGAC	127		
DB	187	GAGCGCCCGGAGATGAACCTTACAGGTGGGTTTCAAGCGCTCTAAGGGAGATCGGACAC	246		
QY	128	ATGATATACTTGGAAAAGCACTATCTGTCCACTTGCCTAGAGATTTCAAGAGCTT	187		
DB	247	ATGGACAACTTGGAGAGACACTCATTTGGCCCATCTGCCCTGGAGATTTTCTCAAGGCC	306		

OY	188	GTGGTCATCTTCCTCCCTTGCCAGCAACA	CTGTGCAAGAAATGTCGATGACATCTTCCAG	247
Db	307	GTGGTGATCTTGGCCCTGCGCAACAAC	CTGTGCGCGCAAGTGTGCCAACACAGCTTTCAG	366
OY	248	GCCTCTAACCCCGTACTTAAACCAAGAGG	CAACACCGTGGCATCAGGGGGCCGCTTC	307
Db	367	GCCTCTAATCCTCTGTGGCAATCCGGGG	CTCCACAAGGTGTCTTCAAGAGACGTTTC	426
OY	308	CGCTGTCCCTCCTGACACATGAGTGTGT	TAGACAGACATGGGGTCTATGACCTGCAG	367
Db	427	CGATCCCACTTGTGATAGGACAGAGGT	GTCTCGSACAGGCATGTGTCTATGGCCTCAG	486
OY	368	AGGAACCTGCTGTGTGAAAACATTAATG	ATATCAACAGAAATCCACAGGCCA----	424
Db	487	CGAAACCTGTGATGTGAGAAATCATTTG	ACATTCACACAGGAGTCTTCGCGGCACATG	546
OY	425	---GAAAAAAATTTGACCCAGCCCATG	TGTGAAGACATGAAGAGAAAGCATCAATCC	481
Db	547	CACGCCAAGCGTGAACACGACCTCAATG	TGTGAGAGCAAGAGAACAAAGATCAACATC	606
OY	482	TATTGTCTGAACCTGTGAAGTGCCAC	CTGTGTTCTTGTGCAAGTTTTTGGCGCCATAG	541
Db	607	TACTGCCCTGAGCTGGAGGTGCCCCAC	CTGTCTCTCTGCAAGGTTTTCCGCGCCCAAG	666
OY	542	GACTGCCAGGTGGCTCCCCCTGACTCAT	GTGTTCCAGAGCAGAAAGTCACAGCTCAAGTAT	601
Db	667	GACTGTGAGTGGGCCCTTGGCCACCA	TTTACAAAGCCAGAAAGTGAAGCTGACCGAT	726
OY	602	GGTATCTGCTGATCTTGTGGAAGCA	CGATAGAGTCAGAGGTGTGATCAAGCCAGCTGAG	661
Db	727	GGCATCGCGATGCTGCTGGCGGGCA	TGACCGTGTCAAGGACGTATCAACCGATGAG	786
OY	662	GACACCTGTAAAACTATTGAGAGTCTG	CAGAAAGCAAGAACAGGACCTGTGTAGAAA	721
Db	787	GAGGTGTGCAACCATTTGAGAGCAAC	AGCCCCAGACAAAGACACTGTTAAACCGAAG	846
OY	722	TTTGTATCAACTTAAAGGCACTCTCG	AGAGAGAAAGACTGAATGACCCAGGCATCACT	781
Db	847	TTTCGAGACCTCTGTGGCGGTTTTT	TGAGAGAGCCGAAAGGCGAACTCTTCAAGCATGGCC	906
OY	782	CGAACACAGAGAGAGAACTGGAACAT	GTCCGAACCTCTTATCAGAAATATCCGATCAC	841
Db	907	CGGGAGCAGAGAGAAAGATTGCAG	CGCGTGGGGGCTCATCGCAGATACGAGAACAC	966
OY	842	CTGAGAAACGTATCCAGTTGGTGGAT	TAGAGAAATCCATTTCATGATAGAGCCCAAAAG	901
Db	967	TTGGAGGGCTCTCTCAAAAGCTGTG	TGAGTCCGCGATCAATTCATGAGAGAGCCGAGATG	1022
OY	902	GCAGTAATTTCTGCAGAATGCCAAAG	CCCTGTGGCAAAAGATCGTGGAAACATCAAGGCG	961
Db	1027	GCTCTCTACCTCCAGAGGCCAAGAG	CGTGAATCAAAAGTCCGGGCCAATGTGAAAGTGTG	108
OY	962	TTTTCAGATGAGAAACCTAGAACAG	GGTATAGAGATATAGCAACTTCACTGTCAATCTC	102
Db	1087	GAGCTGGACAGGACCGGCCGAGAC	CGAGCTATGAGAGCATGAGCAATTTCTCTGAGACGTG	114
OY	1022	AATAGAGAAAGAAAAATTTATCCGT	GAATTTGACTTTTACAGAAAGAGAAAGAGAAAGAA	108
Db	1147	GAGCAGCTGGCCGAAATGTTGGAA	ACATCGAATTTCCAGCCGGGCCCCCTGGGGATGAA	120
OY	1082	GATGACAGAGAAATGATGAAGAAAG	AGAGAGAGATGCAAGTATAGAAATGAGAGGCA	114
Db	1207	GAGGATGACGACATGGCTTTGAT	TGGGAGGAGAGGCAATGTGGCGCTGTGAGAGAGAGCGG	126
OY	1142	GAAATGTTCAAATGACATC	1161	
Db	1267	CTGACGTGCCAGAAAGGCTC	1286	

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? Patent No.6740751
? GENERAL INFORMATION:
? APPLICANT: OLSON, ERIC
? APPLICANT: SPENCER, JEFFREY A.
? TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
? TITLE OF INVENTION: IN STRIATED MUSCLE CELLS
? FILE REFERENCE: WYOG:028US
? CURRENT APPLICATION NUMBER: US/09/908, 988B
? CURRENT FILING DATE: 2000-07-18
? PRIOR APPLICATION NUMBER: 60/219, 020
? PRIOR FILING DATE: 2000-07-18
? NUMBER OF SEQ ID NOS: 6
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 5
? LENGTH: 1597
? TYPE: DNA
? ORGANISM: Mus musculus
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (299) ..(1327)
? US-09-908-988B-5

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Query Match	16.7%	Score 432.2	ID 42	Length 1597
Best Local Similarity	66.5%	Pred. No. 1.3e-118		
Matches 636	Conservative 0	Mismatches 318	Indels 3	Gaps 1
QY	126	CCATGGAATTAACCTTGGAAAGCAACCTGATCTGTCCTCCATCTGCTAGAGATGTTCCAGAAC	185	
DB	336	CTATGGAGAACCTGGAGAGACAGCTGATCTGCCCCATCTGCTGGAGATGTTTACCAAGC	395	
QY	186	CTGTGGTCATTTCTCCCTTGGCCAGACAAACCTGTGACAGAAATGTCCAGTGACATCTTCC	245	
DB	396	CTGTGGTCATCTCTCCCTGCCAACACAACTCTGTCCGGAAGTGTGCCAAGACATCTTCC	455	
QY	246	AGGCTCTAACCCGCTACTTACCCCAAGAGAGGACACCCGTGACATCAGGGGGCCGCT	305	
DB	456	AGGCTGGGAATCCCTCATCGAACCAACCGCGGTGGCTAGTGTCCATGTGGAGGTGTT	515	
QY	306	TCCGCTGTCCCTCCCTGACACATAGGTGGTGTAGACAGACATGGGGTCTATGAGCTGC	365	
DB	516	TCCGTTGCCCTCTGTCGCCCATTAAGTATGATCATGACCCGGACGGGTGTACGGCCTGC	575	
QY	366	AGAGAAACCTGCTGTGGAAAAACATTATTGATATCTAACAGCAGAAATCCACCA--GCG	422	
DB	576	AGAGAAACCTGCTGTGGAAAAACATATTGATCATCAAGCAGAAATGCTCCAGTGGCG	635	
QY	423	CAGAAAAAAATTTGACCAAGCCCATGTGTGAAGGCAAGAAAGAAACGATCAACATCT	482	
DB	636	CCCTGCAAAAAGGACAGCCACCCGATGTGCAAGAAACGAAAGCAGAAAGATCAACATCT	695	
QY	483	ATTGTGCAACTGTGAAGTGGCCACCTGTTCCTGTGSCAAGTTTGGGGCCCATTAAG	542	
DB	696	ACTGTCTCACGTGGAAGGTGCTACTTGTCTCTGTGSCAAGGTGTTGGGCTTCCAGG	755	
QY	543	ACTGCCAAGTGGCTCCCTCTGACTCATGTGTGTCCAGAGCAGAAATCAGACTCAGTATG	602	
DB	756	CCTGTGAAGTGTGGCCCTTTGGCAAGCATCTTCCAGGACAGAAAGATCAGAGTGATTA	815	
QY	603	GTATTGCTGTACTTTGTGGGAAGCAACGATAGAGTCCAGGCTGTGATACGACGCTGAGG	662	
DB	816	GCATCTCCATGCTGTGTGGCGGGGAACGACGAGTGCAGAGATCATCTCTACGCTGAGG	875	
QY	663	ACACCTGTAAAACTATTGAGSAGTGTGCGAAGAAACGAAACGAACTGTGTGGAAT	722	
DB	876	ACTGTGTGAAGTGAACCAAGAGAAATAGCCAACGAGTGAAGAGAGACTGATGCAAGT	935	
QY	723	TTGATTCACCTTAAGGCGATCCTGGAGAGAGAAAGCTGAATATGACCCAGACCATCTC	782	
DB	936	TTGACACCCCTTAAGCCATCTGTGATGAAGAAAGACGACGCTCTGCAAGCATCAAGC	995	
QY	783	GAAACAAGAGAGAAACTGGAACATGTCCGAACCTTATTCAGGAAGTATTTCCATACC	842	
DB	996	AGGAGACGAGAGAAACTGGGCTTTCATTCAGAGCTGTGATCTTCACTTACAGGAGAGC	1055	


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RESULT 7
US-09-949-016-15195
; Sequence 15195, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15195
; LENGTH: 4843
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15195

Query Match      2.8%; Score 73.6; DB 4; Length 4843;
Best Local Similarity 67.8%; Pred. No. 9.3e-10;
Matches 103; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Oy      765 TGACCCAGCATCTCTGGAACACGAGGAGAAATGGAACATCTCCGAATCTTATCA 824
Db      4   TGTCTGACGCGCTGCGCGGAGCAAGAGAACTGACGCGCTCCGCGCTCATCC 63

Oy      825 GAAAGTATTCGATCACTCGAGACCTGGAACATGATCAATGTTGTGAGTCAAGAAATTCAGTTCA 884
Db      64   GTCACTATGGGACCACTCGAGGCTCTCTTAAGCTGTGAGTCTCCATCCAGTCCA 123

Oy      885 TGGATGAGCCCGAAATGCGACGATTTCTGCAG 916
Db      124 TGAAGAGCCCAAAATGCGCGCTATCTCCAG 155

RESULT 8
US-09-949-016-14581/c
; Sequence 14581, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14581
; LENGTH: 64309
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(64309)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14581

Query Match      2.7%; Score 71.2; DB 4; Length 64309;
Best Local Similarity 61.2%; Pred. No. 2.6e-08;
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Matches 115; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Oy      1009 CACTGTCATCTCAATAGAGAGAAAAATTTATCCGTGAATGACTTTTCTAGAGAGA 1068
Db      24085 CAGAGCCAAATCTCATAGAGAGAGAGAGTGAAGAGAGAGAGAGAGAGAGA 24026

Oy      1069 GAAAGAGAAAGATGTCAGAGAAATATGATGAAGAGAGAGAGAGAGTCACTAGA 1128
Db      24025 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 23966

Oy      1129 AGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1188
Db      23965 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 23906

Oy      1189 AGCTGCAG 1196
Db      23905 AGAAGAGAG 23898

RESULT 9
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHRIFFLINER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMTU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F15
US-08-232-463-14

Query Match      2.7%; Score 69.8; DB 1; Length 7218;
Best Local Similarity 2.1%; Pred. No. 1.5e-08;
Matches 8; Conservative 235; Mismatches 132; Indels 0; Gaps 0;

Oy      2216 AGGCGACTGTAGAGGTTCTTTCCTATGAGATCCATGGGTGCGAGACGAGACTTTCCT 2275
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Sequence: 1 ccgagattacccttaccag.....ccctctctctctctcc 2590

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6046767 seqs, 3099530249 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2590	100.0	2590	19	US-10-775-649-3
3	2590	100.0	2590	19	US-10-775-627-3
4	1266.4	48.9	1925	17	US-10-104-047-673
5	910.8	35.2	2434	19	US-10-473-574-36
6	910.8	35.2	2634	17	US-10-104-047-433
7	910.8	35.2	2662	20	US-10-723-860-7135

8	899.8	34.7	1762	9	US-09-764-864-34	Sequence 34, Appl
9	485.6	18.7	2110	21	US-10-204-921-12	Sequence 12, Appl
10	461	17.8	1913	10	US-09-890-668-57	Sequence 57, Appl
11	452	17.5	1053	15	US-10-061-043A-20	Sequence 20, Appl
12	452	17.5	1053	17	US-10-060-634C-20	Sequence 20, Appl
13	450.8	17.4	1431	9	US-09-908-988B-1	Sequence 1, Appl
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16	440.8	17.0	2097	15	US-10-061-043A-22	Sequence 22, Appl
17	440.8	17.0	2097	17	US-10-060-634C-22	Sequence 22, Appl
18	439.2	17.0	1764	17	US-10-094-749-1222	Sequence 1222, Ap
19	439.2	17.0	1764	17	US-10-221-625-192	Sequence 192, App
20	439.2	17.0	1764	18	US-10-723-860-7801	Sequence 7801, Ap
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38	140.4	5.4	1039	9	US-09-880-192-25	Sequence 25, Appl
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ALIGNMENTS

RESULT 1
US-09-908-988B-3
Sequence 3, Appl1
Patent No. US20020127690A1
GENERAL INFORMATION:
APPLICANT: OLSON, ERIC
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
FILE REFERENCE: MYOG:028US
CURRENT APPLICATION NUMBER: US/09/908,988B
CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/219,020
PRIOR FILING DATE: 2000-07-18
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 2590
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (80) .. (1714)
US-09-908-988B-3

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Best Local Similarity 100.0%; Pred. No. 0;
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; Publication No. US20040132160A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; TITLE OF INVENTION: AND INTERMEDIATE FILAMENTS IN STRIATED MUSCLE CELLS
; FILE REFERENCE: WMOG-028USD2
; CURRENT APPLICATION NUMBER: US/10/775,649
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 09/908,988
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
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; TYPE: DNA
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Db	1801	ATATGAAGGGGACCTCTGAGACGATTTCTGAAGCAAAACAAAACAATACACACACC	1860
Qy	1861	ACCCTTTAATTCAGATGACTTATCTCACTCATTTGAGAAATGATATGCTCAGAACAA	1920
Db	1861	ACCCTTTAATTCAGATGACTTATCTCACTCATTTGAGAAATGATATGCTCAGAACAA	1920
Qy	1921	ATTACAGAAATACTCTTCTGAGAGAACTTGATCTTCTGCAAACTTTCAATTTGTGAG	1980
Db	1921	ATTACAGAAATACTCTTCTGAGAGAACTTGATCTTCTGCAAACTTTCAATTTGTGAG	1980
Qy	1981	AAACCTTCTGAAGTGTGTAGTGTGTGTGCACTGCTGTGATCAGCCATATAGTGCAG	2040
Db	1981	AAACCTTCTGAAGTGTGTAGTGTGTGTGCACTGCTGTGATCAGCCATATAGTGCAG	2040
Qy	2041	TGTTAAACAAAGTGCAGAACTCTCCAGCCTCCCTCAGGCTCTGGTTATTTTAGGAC	2100
Db	2041	TGTTAAACAAAGTGCAGAACTCTCCAGCCTCCCTCAGGCTCTGGTTATTTTAGGAC	2100
Qy	2101	GCTTGTGCTTTTGCTTTTCTCTTAGCATTGCAAGTGTAGTGTGATGTCAGTGTAGT	2160
Db	2101	GCTTGTGCTTTTGCTTTTCTCTTAGCATTGCAAGTGTAGTGTGATGTCAGTGTAGT	2160
Qy	2161	TCCAAACTGACCCGATTATCAAAATATGAGATTTGTCACTGACCAAAAGCTATGAGGC	2220
Db	2161	TCCAAACTGACCCGATTATCAAAATATGAGATTTGTCACTGACCAAAAGCTATGAGGC	2220
Qy	2221	ACTGAGAGGTTCCTTTTCCCTATGATGTCATGGGTGTGCGACAGGACTTTCCTTACA	2280
Db	2221	ACTGAGAGGTTCCTTTTCCCTATGATGTCATGGGTGTGCGACAGGACTTTCCTTACA	2280
Qy	2281	TGTGGCCACAGTCCATATGTCAGAAAGCCAAAATCTAGGGCAACTCTTTTGACATTTT	2340
Db	2281	TGTGGCCACAGTCCATATGTCAGAAAGCCAAAATCTAGGGCAACTCTTTTGACATTTT	2340
Qy	2341	TCATACTTATTTACATATCTCATATATATATCCATGTATTAGGCAATTTAATGAATTT	2400
Db	2341	TCATACTTATTTACATATCTCATATATATATCCATGTATTAGGCAATTTAATGAATTT	2400

Db	2341	TCGTAACCTTATTACATATCTGATATCATATCATATCATATGATATTAGGACATTTTAATTAATGAATTT	2400
QY	2401	CAAGAAGAGCGCTGTCTACTTTCTTAAGTGTCTGCGCATPAGACAGCAATCTGATATCTGTG	2460
Db	2401	CAAGAAGAGCGCTGTCTACTTTCTTAAGTGTCTGCGCATPAGACAGCAATCTGATATCTGTG	2460
QY	2461	GAGCAACCTGCAATGATTTAAGTATACACAAATCTCCCTGTGATGACCTTCTCTCTC	2520
Db	2461	GAGCAACCTGCAATGATTTAAGTATACACAAATCTCCCTGTGATGACCTTCTCTCTC	2520
QY	2521	TCCTCTCTCCCTCTCTCCCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2580
Db	2521	TCCTCTCTCCCTCTCTCCCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2580
QY	2581	TTCTTCTCTCC 2590	
Db	2581	TTCTTCTCTCC 2590	
RESULT 3			
US-10-775-627-3			
; Sequence 3, Application US/10775627			
; Publication No. US20040142446A1			
; GENERAL INFORMATION:			
; APPLICANT: OLSON, ERIC			
; APPLICANT: SPENCER, JEFFREY A.			
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES			
; TITLE OF INVENTION: AND INTERMEDIATE FILAMENTS IN STRIATED MUSCLE CELLS			
; FILE REFERENCE: WMOG-028USD1			
; CURRENT APPLICATION NUMBER: US/10/775,627			
; CURRENT FILING DATE: 2004-02-10			
; PRIOR APPLICATION NUMBER: 09/908,988			
; PRIOR FILING DATE: 2001-07-18			
; PRIOR APPLICATION NUMBER: 60/219,020			
; PRIOR FILING DATE: 2000-07-18			
; NUMBER OF SEQ ID NOS: 6			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 3			
; LENGTH: 2590			
; TYPE: DNA			
; ORGANISM: Mus musculus			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (80)..(1714)			
US-10-775-627-3			
Query Match 100.0%; Score 2590; DB 19; Length 2590;			
Best Local Similarity 100.0%; Prid. No. 0;			
Matches 2590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	CTCGAGATTATCCCTTACAGAAAGCTGTTCGGGAGACACTTTCCTTGGAGACACTCTAG	60
Db	1	CTCGAGATTATCCCTTACAGAAAGCTGTTCGGGAGACACTTTCCTTGGAGACACTCTAG	60
QY	61	GGAACAGGACGGCAAGAAATGAGCACTTCTGTAATTACAGTCTTTCTCCAAAGACA	120
Db	61	GGAACAGGACGGCAAGAAATGAGCACTTCTGTAATTACAGTCTTTCTCCAAAGACA	120
QY	121	GCAAGCACTGATTAATCTGGAAAAACAATGATTTGTCCTCATCTGCTAGAGATTTTAC	180
Db	121	GCAAGCACTGATTAATCTGGAAAAACAATGATTTGTCCTCATCTGCTAGAGATTTTAC	180
QY	181	GAAAGCTGTGTGATTTCTCCCTTTCGAGCAACCTGTGACAGAAATGTGCGAGTGCAT	240
Db	181	GAAAGCTGTGTGATTTCTCCCTTTCGAGCAACCTGTGACAGAAATGTGCGAGTGCAT	240
QY	241	CTTCAGGCGCTCTAACCCGTAATTACCCACAAGAGAGGACCAACCGTGGCATCAGGGG	300
Db	241	CTTCAGGCGCTCTAACCCGTAATTACCCACAAGAGAGGACCAACCGTGGCATCAGGGG	300
QY	301	CCGCTTCCGCTGTCTCTCTCTGACAGATGAGTGTGTGAGACAGACATGGAGTCTATGG	360
Db	301	CCGCTTCCGCTGTCTCTCTCTGACAGATGAGTGTGTGAGACAGACATGGAGTCTATGG	360

QY 361 ACTGCAGAGAACCTGCTCGTGGAAAAATTATTTATCTAAGAGGAAATCCACAG 420
DB 361 ACTGCAGAGAACCTGCTCGTGGAAAAATTATTTATCTAAGAGGAAATCCACAG 420
QY 421 GCCAGAAAAAAATTGGACGACCCTATGTGTGAAGAGCATGAAGAGAAAGCATCAACAT 480
DB 421 GCCAGAAAAAAATTGGACGACCCTATGTGTGAAGAGCATGAAGAGAAAGCATCAACAT 480
QY 481 CTATTTGCTGAACCTGTGAAGTGGCCACCTGTCTTGTGCAAGGTTTTTGGCCCATAA 540
DB 481 CTATTTGCTGAACCTGTGAAGTGGCCACCTGTCTTGTGCAAGGTTTTTGGCCCATAA 540
QY 541 GGAATGCGAGTGGTCCCTCCGACTCATGTGTCCAGAGGCAAGAGCATGAGTCAAGTGA 600
DB 541 GGAATGCGAGTGGTCCCTCCGACTCATGTGTCCAGAGGCAAGAGCATGAGTCAAGTGA 600
QY 601 TGGTATTTGCTGTACTTGTGGGAAGCAAGATAGAGTCAAGGTTGTATCAGCAGCTGA 660
DB 601 TGGTATTTGCTGTACTTGTGGGAAGCAAGATAGAGTCAAGGTTGTATCAGCAGCTGA 660
QY 661 GGAACCTGTAAACCTATTTAGAGAGTCTGCAAGAACAGAAACAGGACCTGTGTGAAA 720
DB 661 GGAACCTGTAAACCTATTTAGAGAGTCTGCAAGAACAGAAACAGGACCTGTGTGAAA 720
QY 721 ATTGTATCAGCTATACCGGCAATCTGTGAGAGAGAGAAAGATGAATGATCCAGCATCAC 780
DB 721 ATTGTATCAGCTATACCGGCAATCTGTGAGAGAGAGAAAGATGAATGATCCAGCATCAC 780
QY 781 TCGAACAAGAGAGAGAACTGGAACATGTCCGAACCTTATCAGAAAGTATTCCGATCA 840
DB 781 TCGAACAAGAGAGAGAACTGGAACATGTCCGAACCTTATCAGAAAGTATTCCGATCA 840
QY 841 CCTGGAAGACGTATCCAAAGTTGTGAGTCAAGAAATCAGTTCAATGAGTCCGAAAT 900
DB 841 CCTGGAAGACGTATCCAAAGTTGTGAGTCAAGAAATCAGTTCAATGAGTCCGAAAT 900
QY 901 GGCAGATATTTCTGCAAGATGCGCAAGACCTGTGTCAAAAAGATGTGGAAGCATCAAGGC 960
DB 901 GGCAGATATTTCTGCAAGATGCGCAAGACCTGTGTCAAAAAGATGTGGAAGCATCAAGGC 960
QY 961 GTTTCAGATGGAAGAACTAGAAACAAGTTATGAGATCATGAGCACTTCACTGTCAATCT 1020
DB 961 GTTTCAGATGGAAGAACTAGAAACAAGTTATGAGATCATGAGCACTTCACTGTCAATCT 1020
QY 1021 CAATAGAGAAAGAAAAATTATCCGTGAATTTGACTTTTCTAGAGAAAGAGAGAAAGA 1080
DB 1021 CAATAGAGAAAGAAAAATTATCCGTGAATTTGACTTTTCTAGAGAAAGAGAGAAAGA 1080
QY 1081 AGATGCGAGAGAAATAGATGAAGAAAGAGAGAGATGCAATGAGATGAAGAGGC 1140
DB 1081 AGATGCGAGAGAAATAGATGAAGAAAGAGAGAGATGCAATGAGATGAAGAGGC 1140
QY 1141 AGAAAAATGTTCAATATAGCATCTTCAGGGGAAAGAGAGAGTGTGAGAAAGCTGCAAGGC 1200
DB 1141 AGAAAAATGTTCAATATAGCATCTTCAGGGGAAAGAGAGAGTGTGAGAAAGCTGCAAGGC 1200
QY 1201 CTCTCAGCTTCCCGCAGAGCTTCAGATCGGCCCAAGCACTACCTGCTTCTCCAGA 1260
DB 1201 CTCTCAGCTTCCCGCAGAGCTTCAGATCGGCCCAAGCACTACCTGCTTCTCCAGA 1260
QY 1261 ACCGTTTTCATCCATGCGACCTGTCAGATGTCTGTGTGACACAGGGGGAGGTGTGCC 1320
DB 1261 ACCGTTTTCATCCATGCGACCTGTCAGATGTCTGTGTGACACAGGGGGAGGTGTGCC 1320
QY 1321 CATTTGCTCAGCAGACACAGCTGAAAATTCTCAGGCCCTTCAAGCAGGAGAACTGC 1380
DB 1321 CATTTGCTCAGCAGACACAGCTGAAAATTCTCAGGCCCTTCAAGCAGGAGAACTGC 1380
QY 1381 GGATCCCTTGTTTTAACTAGTTGTATTAAGGCCAAGCCGAGAAACAGCTTCAACCC 1440
DB 1381 GGATCCCTTGTTTTAACTAGTTGTATTAAGGCCAAGCCGAGAAACAGCTTCAACCC 1440

QY 1441 ACCTGCACTCATGGAGTGAAGGTCTGGGTCAAAATAGGAGCCTTGGGCAATGAGATTC 1500
DB 1441 ACCTGCACTCATGGAGTGAAGGTCTGGGTCAAAATAGGAGCCTTGGGCAATGAGATTC 1500
QY 1501 CAGTGTGCACTCCGAGAAAGTGGCAGAAAGCCGCAACCAATGAGCAGCAGTGAATGG 1560
DB 1501 CAGTGTGCACTCCGAGAAAGTGGCAGAAAGCCGCAACCAATGAGCAGCAGTGAATGG 1560
QY 1561 TAAAGATGTAAGTTCAACTGCAAGTACTCTCTCAGATTTGATTTGAGCCCTTCTCCCA 1620
DB 1561 TAAAGATGTAAGTTCAACTGCAAGTACTCTCTCAGATTTGATTTGAGCCCTTCTCCCA 1620
QY 1621 GGGACAGTCCGAGCCTTGGGGAGTGGGGGTGGGGATCTGAGCAGCAGTCCGACGTC 1680
DB 1621 GGGACAGTCCGAGCCTTGGGGAGTGGGGGTGGGGATCTGAGCAGCAGTCCGACGTC 1680
QY 1681 TTCTCCTTCTCTGTGTTGAATTCCTTAATGAAATTAATTTATCTGTGTCGCCCC 1740
DB 1681 TTCTCCTTCTCTGTGTTGAATTCCTTAATGAAATTAATTTATCTGTGTCGCCCC 1740
QY 1741 TGTCTGCTGTGTTGAAGACATGAGGACAGAGAAACAGTGTGAATTTCAACGATTC 1800
DB 1741 TGTCTGCTGTGTTGAAGACATGAGGACAGAGAAACAGTGTGAATTTCAACGATTC 1800
QY 1801 ATATGAAGGGGACCTCTGACAGGATTTCTGAAGCAAAACAAATACAAACACACC 1860
DB 1801 ATATGAAGGGGACCTCTGACAGGATTTCTGAAGCAAAACAAATACAAACACACC 1860
QY 1861 ACCCTTAAATTCAGATGACTTATCTCACTCATTTGAAAAATGATTTATGTCAGAACAA 1920
DB 1861 ACCCTTAAATTCAGATGACTTATCTCACTCATTTGAAAAATGATTTATGTCAGAACAA 1920
QY 1921 ATTACAGAAATATCTCTTCTGAAGAACTTGAATCTTCTGCAATCTTTCAATTTGTGTAG 1980
DB 1921 ATTACAGAAATATCTCTTCTGAAGAACTTGAATCTTCTGCAATCTTTCAATTTGTGTAG 1980
QY 1981 AAACCTTGAAGGTGTGTGAGTGTGAGTGTGCAATGCTGTGTATCAGCAATTAAGTGCAG 2040
DB 1981 AAACCTTGAAGGTGTGTGAGTGTGAGTGTGCAATGCTGTGTATCAGCAATTAAGTGCAG 2040
QY 2041 TGGTAAACAAAGTGGCAGAAACACTCTCCAGCCTCCCTCAGGCTTCTGTATTTATTTAGAC 2100
DB 2041 TGGTAAACAAAGTGGCAGAAACACTCTCCAGCCTCCCTCAGGCTTCTGTATTTATTTAGAC 2100
QY 2101 GCTTGTGCTTTTCTTTTCTCTTCTGATGCAATGAGGTGATGATTTCACTGATCAGT 2160
DB 2101 GCTTGTGCTTTTCTTTTCTCTTCTGATGCAATGAGGTGATGATTTCACTGATCAGT 2160
QY 2161 TCCAACTGACCGATTTATCAAAATATGAGATTTGCTCATGACCAAGCTATGTAGGC 2220
DB 2161 TCCAACTGACCGATTTATCAAAATATGAGATTTGCTCATGACCAAGCTATGTAGGC 2220
QY 2221 ACTGTAGAGTTCCTTCCCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
DB 2221 ACTGTAGAGTTCCTTCCCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
QY 2281 TGTGGCACAAGTCCATAGTCCAGAAAGCCAAAATCTAGGGCACTCTTTTGAACATTT 2340
DB 2281 TGTGGCACAAGTCCATAGTCCAGAAAGCCAAAATCTAGGGCACTCTTTTGAACATTT 2340
QY 2341 TCTTAACCTTATTAATCAATCTCATATCATATCATATCATATCATATCATATCATATTAAT 2400
DB 2341 TCTTAACCTTATTAATCAATCTCATATCATATCATATCATATCATATCATATCATATTAAT 2400
QY 2401 CAAAGAGAGCTGTCTACTTCTTAAAGTCTCTGATAGCAGCAATCTGATTAATCTGTG 2460
DB 2401 CAAAGAGAGCTGTCTACTTCTTAAAGTCTCTGATAGCAGCAATCTGATTAATCTGTG 2460
QY 2461 GAGCAACTGATGATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2520
DB 2461 GAGCAACTGATGATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2520
QY 2521 TGTCTGCTCCCT 2580

OY		1191	CTGAGAGACCCTTCAGCTTCCCGAGAAGTTCAAGTGCCACAGACCATCCTGGTT	1258
Dd		1210	CTTAGAGACTCTTCAG-----GGGAGCTGCAGAGCTGCCCTGTGGGCACTTCCAATT	1363
OY		1251	CCTCTCCGAACCGTTTTTCATTCATGCACCTGCTGCAGATGTCTGTGTACAAG	1306
Dd		1364	CCTCTCCAGAACCACTCCAGCCCCTGCACCTGTCTGGATGCCCCCTGTGACACAG	1419
 RESULT 6 US-10-104-047-433 ; Sequence 433, Application US/10104047 ; Publication No. US20030236392A1 ; GENERAL INFORMATION: APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: No. US20030236392A1el full length cDNA FILE REFERENCE: H1-A0105 CURRENT APPLICATION NUMBER: US/10/104, 047 PRIOR FILING DATE: 2002-03-25 PRIORITY APPLICATION NUMBER: NUMBER OF SEQ ID NOS: 4096 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 433 LENGTH: 2634 TYPE: DNA ORGANISM: Homo sapiens US-10-104-047-433				
 Query Match 35.2%; Score 910.8; DB 17; Length 2634; Best Local Similarity 84.2%; Pred. No. 1,3e+24; Matches 1058; Conservative 0; Mismatches 177; Indels 21; Gaps 2;				
OY		66	GGAAGCGCAAGAAATGAGCACTTCTGTGAATTACAGTCTTTTCCAAAGACAGCAGA	125
Dd		363	GGGACAGCGAGAGATGAGCCGATCTGTGAATTACAATCTTTTTCCAAAGACAGCAGA	422
OY		126	CCATGSAATACTTGAAAAAGAACMGATCTGTCCCATTTGCTTAAGATGTTACAGAGC	185
Dd		423	CAAATGSAATACTTGAAAAGAACCACTGTGTCCTCATGTCTTAAGATGTTACAGAAAC	482
OY		186	CTGTGTGTCATTCTCCCTTGCAGACCAACTGTGTGAGAAAAATGTSCAGTGACATCTCC	245
Dd		483	CTGTGTGTCATTCTCCCTTGTGAGACCAACTGTGTGAGAAATGTGCCAGTGATATTTTCC	542
OY		246	AGGCTCTTAACCCGTCATTACCCACAMAGAGAGCACCACTGTGCATCAGGGGCGCT	305
Dd		543	AGGCTCTTAACCCGTCATTATGGCCACAMAGAGAGTACCACCATGTGCATCAGGGGCGAT	602
OY		306	TCCGCTGTCCCTCTCTGCGAGACATGAGGTGTGTGTGACAGACATGTGGGTCTATGATGCG	365
Dd		603	TCCGCTGTCCCATCTCGTGAACATGAAAGTGTGTGTGATGACATGTGGGTATATGATCTTC	662
OY		366	AGAGGAACCTCTCGTGTGAAAAACATTA TTGATATCTTACAGAGGAAATCCACACAGGCGAG	425
Dd		663	AGAGGAACCTCTCGTGTGAAAAATATCATTTGATACATTA CAAGCAGAGATCCACAGGCGAG	722
OY		426	AAAAAAAAATTGACACAGCCCATGTGTGAAGACATGAAGAGAAAGCATCAACTATATT	485
Dd		723	AAAAAATATCGAACACAGCCCATGTGTGAGAAACATGAAGAGAGGACATCAACTATCTACT	782
OY		486	GTCTGAACCTGTGAAGTGTGCCAACCTGTCTCTGTGTGAAGTTTTGTGGCCCATAGAGACT	545
Dd		783	GTCTGAACCTGTGAAGTATCCCACTGTGCTTCTGTGTGAAGTGTGTGTGTGACACAAGACT	842
OY		546	GCCAGGTGTGTCCTCCCTGACTCATGTGTCCAGAGGACAGAAATGACAGTCAATGTGTA	605
Dd		843	GCCAGGTGTGTCCTCCCTCATGTGTCTTCCAGAGACAGAAATGTGAGCTCAATGTGTGCA	902
OY		606	TTCGTGTACTTGTGTGAAGCAACGATAGAGTCCAGGATGTGTATCGCCAGCTGTGAGACA	665
Dd		903	TTCGCATCTCTGTGGGAGCAACGATGAGTTCAGAGAGTATCATAGCTGTGTAAGACA	962

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QY 666 CCTTAAACATATGAGAGGTGCTGCGAGAAAGAGAAACAGACACTGTGTGAGAAATTTG 725
Db 963 CCTCGAAAATCTATCGAGGAATGTTTGCAGAAAACAGAAACAAGACCTTTGTGAGAAAGTTTG 1022
QY 726 ATCACTATTACGGGATCTGTGAGAGAGAGAAAGACTGAATATGACCCAAAGCCATCACTTGAA 785
Db 1203 ATTACTGTATATGGCATTTTGTGAGAGAGAGAAATGAATGACCCAAATGATTAACCGGAA 1082
QY 786 CACGAGAGAGAAACTGTGAACATGTCCGAACTCTTATCAGAAAGTATTTCCGATCACTGG 845
Db 1083 CCGAAGAGAGAAACTGGAACATGTCCGTCTCTGATCAAAAAAGTATTCGATCATTTTG 1142
QY 846 AGAAGCATATCCAAAGTTGTGTGAGTCAAGAAATCCAGTTCATGATAGAGCCGGAATATGCGAG 905
Db 1143 AGAAGCATATCCAAAGTTGTGTGAGTCAAGAAATTCAGTTTATGATAGAGCCGGAATATGCGAG 1202
QY 906 TATTTCTGCAGAAATGCCAAGACCTCTTTGCAAAAAGATCGTGAAGCATCAAGGCGCTTTC 965
Db 1203 TGTTTCTGCAGAAATGCCAACCCTGCTTAABAAAAATCTGGAAGACATCAAGGCATTTTC 1262
QY 966 AGATGAGAAACTATGAACAAGTTTATGATCATGAGCAACTTCACTGTCAATCTCAATA 1025
Db 1263 AGATGAGAAAAATGAAACATGCGTATGAGAACATGAACCACTTCAAGTCAACTCAATA 1322
QY 1026 GAGAAAGAAAAAATATTCGGTGAATTTGACCTTTCTAGAGAAAGGAAGAGAAAGAAATG 1085
Db 1323 GAGAAAGAAAAATATATACGTGAATTTGACCTTTTACAGAGAAATGAAGAAAGAAAGAAAG 1382
QY 1086 CAGAGAAATATGATGAAGAAAGAGAAAGAGA-----GAGTCAGTAGAG 1130
Db 1383 AAGAAAGCGAGAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTGGAGAGAAAGCAGTAGAG 1442
QY 1131 TAGAAGAGCGAGAAATGTTCAATATAGCATCTTCAGGGGAAAGAGAGAGTCTGAGAGAAAG 1190
Db 1443 TGAAGAGAGTAGAAGAAATGTTCAACAGAGTTCAGAGAGAAAGTGAAGAAACCCGAAAGAAAG 1502
QY 1191 CTGAGAGCCCTCTCAGACTTCCGCGAAGCTTACAGTTCGCCCCAGAGCCACTACCTGCTT 1250
Db 1503 CTTTACAGACTCTCTCAG-----GTGAGAGCTGCAGAGGCTGCCCCCTGGGGCACTTCCAGATTT 1556
QY 1251 CCTCTCCAGAACGTTTTCATTCATTCATGCGCACTGCTGAGATGTCTGTGTACACAG 1306
Db 1557 CCTCTCCAGAGCCACTTCCAGCCCTGCGCACTGCTGCGAGTCCCCGTGTACACAG 1612

RESULT 7
US-10-723-860-7135
; Sequence 7135, Application US/107233860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: Methods for Screening for Soft Tissue Sarcoma Modulators
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/10/723, 860
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7135
; LENGTH: 2662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-7135

Query Match 35.2%; Score 910.8; DB 20; Length 2662;
Best Local Similarity 84.2%; Pred. No. 1,3e-234;
Matches 1058; Conservative 0; Mismatches 177; Indels 21; Gaps 2;

66 GGGAGCGCAGAGAAATAGACATTCTCTGAATTACAAAGCTTTTCTCCAAAGACAGACAGAGA 125

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Db 363 GGGACAGCGAGAGATAGAGCGCATCTCTGAATTACAAATCTTTTCCAAAGACAGAGAGA 422
Qy 126 CCATGATTAATTGAAAAAGCAATGATCTGTCCCACTCCCTAGAGATTTTACCAAGC 185
Db 423 CCATGATTAATTGAAAAAGCAATGATCTGTCCCACTCCCTAGAGATTTTACCAAGC 482
Qy 186 CTGTGTCATCTTCCCTTGCAGACAACTGTGTCAGAGAAATGTCCAGTGCATCTTCC 245
Db 483 CTGTGTCATCTTCCCTTGCAGACAACTGTGTCAGAGAAATGTCCAGTGCATCTTCC 542
Qy 246 AGGCTCTTAAACCCGTAATTAACCAAGAGAGAGCAGCAGTGTGATCAAGGGGCGCT 305
Db 543 AGGCTCTTAAACCCGTAATTAACCAAGAGAGAGTACCAATGATGATGAGGGGCGCT 602
Qy 306 TCCGCTCTCCCTCTGTCAGACATGAGGTGTGTAACACATGGGGTCTATGAGCTCC 365
Db 603 TCCGCTCTCCCTCTGTCAGACATGAGGTGTGTAACATGGGGTCTATGAGCTTC 662
Qy 366 AGAGAACTGTCTGTGAAAAAATTTGATATCTAAGAGAGAAATTCACAGGCGCAG 425
Db 663 AGAGAACTGTCTGTGAAAAAATTTGATATCTAAGAGAGAGTCCACAGGCGCAG 722
Qy 426 AAAAAAATTGACCAAGCCCATGTGTGAGAGAGATGAGAGAAACGATCAATCTATT 485
Db 723 AAAAAAATTGACCAAGCCCATGTGTGAGAGAGATGAGAGAAACGATCAATCTACT 782
Qy 486 GTCTGAATCTGTGAATGCCACCTGTTCTTGTGCAAGGTTTTTGGCCCATAGAGACT 545
Db 783 GTCTGAATCTGTGAATGCCACCTGTTCTTGTGCAAGGTTTTTGGCCCATAGAGACT 842
Qy 546 GCCAGGTCCTCCCTGATCATGTGTTCAGAGGCGAGAGTCAAGACTAGAGTGTGTA 605
Db 843 GCCAGGTCCTCCCTGATCATGTGTTCAGAGAGAGAGTCAAGACTAGAGTGTGTA 902
Qy 606 TTGCTGACTGTGTGAGAGACATAGATCCAGGTCGTGATCAGCAGCTGGAGACA 665
Db 903 TTGCTGACTGTGTGAGAGACATAGATCCAGGTCGTGATCAGCAGCTGGAGACA 962
Qy 666 CTTGTAAATCTATTGAGAGAGTGTGCAAAAAGAGAGAGAGCTGTGTGAGAAATTTG 725
Db 963 CTTGTAAATCTATTGAGAGAGTGTGCAAAAAGAGAGAGAGCTGTGTGAGAAATTTG 1022
Qy 726 ATACCTTAATCGGATCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 785
Db 1023 ATACCTTAATCGGATCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1082
Qy 786 CACAG 845
Db 1083 CACAG 1142
Qy 846 AGAAGCTATCAAGTGTGTGAGAGTCAAGAAATCCAGTTTATGATGAGAGAGAGAG 905
Db 1143 AGAAGCTATCAAGTGTGTGAGAGTCAAGAAATCCAGTTTATGATGAGAGAGAGAG 1202
Qy 906 TATTTTCTGCAAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 965
Db 1203 TATTTTCTGCAAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1262
Qy 966 AGATGAG 1025
Db 1263 AGATGAG 1322
Qy 1026 GAG 1085
Db 1323 GAG 1382
Qy 1086 GAG 1130
Db 1383 GAG 1442
Qy 1131 TAGAAG 1190

Db 1443 TGGAGAGAGTGAAGAAATGTTCAAAACAGAGTTTCCAGAGAGAGTGAAGAAACCCAGAAAAG 1502
Qy 1191 CTGACAGAGCCCTCTGAGTTTCCGAGAGAGCTTTCAGGTCGCCCAAGAGAGAGAGAGAG 1250
Db 1503 CTGACAGAGCCCTCTGAGTTTCCGAGAGAGAGCTTTCAGGTCGCCCAAGAGAGAGAGAG 1556
Qy 1251 CCTCTTCAG 1306
Db 1557 CCTCTTCAG 1612

RESULT 8
US-09-764-864-34
; Sequence 34, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIORITY FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; SOFTWARE: Patentlin Ver. 2.0
; SEQ ID NO 34
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-34

Query Match 34.7%; Score 899.8; DB 9; Length 1762;
Best Local Similarity 84.2%; Pred. No. 9.4e-232;
Matches 1058; Conservative 0; Mismatches 177; Indels 22; Gaps 3;

Qy 66 GGGACGCGAAG 125
Db 143 GGGACGCGAAG 202
Qy 126 CCATGATTAATTGAAAAAGCAATGATCTGTCCCACTCCCTAGAGATTTTACCAAGC 185
Db 203 CCATGATTAATTGAAAAAGCAATGATCTGTCCCACTCCCTAGAGATTTTACCAAGC 262
Qy 186 CTGTGTCATCTTCCCTTGCAGACAACTGTGTCAGAGAAATGTCCAGTGCATCTTCC 244
Db 263 CTGTGTCATCTTCCCTTGCAGACAACTGTGTCAGAGAAATGTCCAGTGCATCTTCC 322
Qy 245 CAGGCTCTTAACCCGTAATTAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 304
Db 323 CAGGCTCTTAACCCGTAATTAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 382
Qy 305 TTCCGCTGTCCCTCTGTCAGACATGAGGTGTGTAACAGAGAGAGAGAGAGAGAGAGAGAG 364
Db 383 TTCCGCTGTCCCTCTGTCAGACATGAGGTGTGTAACAGAGAGAGAGAGAGAGAGAGAGAG 442
Qy 365 CAG 424
Db 443 CAG 502
Qy 425 GAAAAAATTGAG 484
Db 503 GAAAAAATTGAG 562
Qy 485 TGTCTGAATCTGTGAAGTCCCACTGTTCTTGTGCAAGGTTTTTGGCCCAATTAAGAG 544
Db 563 TGTCTGAATCTGTGAAGTCCCACTGTTCTTGTGCAAGGTTTTTGGCCCAATTAAGAG 622
Qy 545 TGCAG 604
Db 623 TGCAG 682
Qy 605 ATTGCTGTACTTGTGAG 664
Db 683 ATTGCTGTACTTGTGAG 742


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Db      688  CACTCAGCTGGAGGATTCGCCGTGAGTGACCAAGAGAAAGTCACCAAGTAAAGAGAA 747
Qy      709  CCTGTGAGAAATTTGATCACTATACGATCTGTGAGAGAGAAAGCTGAATGAC 768
Db      748  GCTGAGCAGAAAGTTTACACGTTGTATGCCATCTGTGATGAGAAAGAGTTGCT 807
Qy      769  CCAAGCCATCACTGCAACAGAGAGAAAGTGAACATGTCGAATCTTTATCAGAA 828
Db      808  GAGCGGATCACGAGAGAGAGAGAAAGTTAGTTACATGAGGCCCTTCATCCAGCA 867
Qy      829  GTATTCGATCACTGAGAAAGTATCCAAAGTTGTGAGTCAAGAAATCCATTCATGA 888
Db      868  GTACCAAGAGAGAGTGGACAAAGTCCACAAAGCTGTGAAACTGCATCCAGTCCCTGGA 927
Qy      889  TGAGCCCGAAATGCGCATATTTCTGCAAGATGCCAAACCTGTGCAAAAGATCCGGA 948
Db      928  CGAGCCCTGGGGAGCCACTTCTCTTGACTGCGCAACCACTCAATCAAAAGCATTTGGA 987
Qy      949  AGCATCAAGGCGCTTTCAGATGAGAAAGTGAACAAAGTTATGATCATGAGCACTT 1008
Db      988  AGCTTCAAGGCGCTGCGAGCTGGGGAGAGACAGAGCAGGCTTTGAGAACATGACTTCTT 1047
Qy      1009  CACTGTCATCTCAATGAGAAAGAAATTTATCCGTGAATTGACTTTTCTAGAGAGA 1068
Db      1048  TACTTGGATTTAGACATATGACAGACGCCCTGAGAGCCATTGACTTTGGAGACAGATGA 1107
Qy      1069  GGAAGAGAAAGAGATCAGAGAAATGATGAAAGAAAGAGAGAGAGATGACATAGA 1128
Db      1108  GGAAGAGAAAGAAATTCATTGAAAGAAAGATCAGAGAGAGAGAGATCCACAGAAAGGAA 1167
Qy      1129  AGTAGAG 1136
Db      1168  GGAAGAG 1175

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RESULT 10
US-09-890-688-57
; Sequence 57, Application US/09890688
; Publication No. US20030144475A1
; GENERAL INFORMATION:
; APPLICANT: Seisshi KATO
; APPLICANT: Chikashi EGUCHI
; APPLICANT: Mihoro SAKI
; TITLE OF INVENTION: Human Proteins and cDNAs thereof
; FILE REFERENCE: 2001-1102A/MMC/00653
; CURRENT APPLICATION NUMBER: US/09/890,688
; PRIOR APPLICATION NUMBER: JP 11-346863
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: JP 11-34684
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: JP 2000-31062
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: JP 2000-34091
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: JP 2000-34090
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: JP 2000-35829
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: JP 2000-35899
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: JP 2000-71161
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: JP 2000-160851
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 1913
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (303) ... (1379)
US-09-890-688-57
Query Match 17.8%; Score 461; DB 10; Length 1913;
Best Similarity 65.0%; Pred. No. 3,4e-113;
Matches 699; Conservative 0; Mismatches 370; Indels 6; Gaps 1;

Qy      62  GACAGGAGCGGCAAGAAATAGACACTTCTGAAATTAACAAGTCTTCCAAAGACAG 121
Db      285  GGCACACACACAGAGGAGATGAATTCACAGTGGTTTCAAGCCGCTCTCAGGGAGTCA 344
Qy      122  CAGACCATGATTAATCTTGAAAGAAACAATGATCTGTCCATCTGCTAGAGATGTTCA 181
Db      345  CACAGATGAGCAACTCGAGAGAAAGAGCTATGTGCCCATCTGCTCGAGATGTTCTCC 404
Qy      182  AAGCTGTGTCATTCTCCCTTCCAGACACACTGTGCAAGAAATGTGCAATGATC 241
Db      405  AAACAGTGTGATCTGCTCCCTCCAAACAACTGTGCGCAAAATGTGCCAACGACGTC 464
Qy      242  TTCCAGGCTCTTAACCCGTAATACCAACAAGAGAGGACCAACGTTGATGAGGGGCG 301
Db      465  TTCAGGCTCTGAATCTCTATGACAGTCCGGGGCTCCACACTGTGTTCAGAGAGGC 524
Qy      302  CGCTCCGCTGTCTCTCTGACAGACATGAGTGTGTTAGACAGACATGAGGCTCTATGA 361
Db      525  CGTTCCGCTGCCCATCTGTGACAGCATGAGTGTCTGTGACAGACACGCTGTCTACGGC 584
Qy      362  CTGCAAGAAAGCTGCTCGTGAAACATTATGATATCTTACAAGCAGAAATCCACAGG 421
Db      585  CTGCAAGAAAGCTGCTGATGAGAAACATTATGATATCTTACAAGCAGAGATCATCAGG 644
Qy      422  CC-----AGAAAAAAATTTGACCAAGCCATGTGTGAAGAGATGAAGAGAACGATC 475
Db      645  CCGCTCACTCCAAAGGCTGACGACCTCATGTGCGAGAGATGAAGAGAAAGATC 704
Qy      476  AACATCTATGTGTGAAGTGTGAAGTGCACCTGTTCTTGTGCAAGTTTGTGGGCGC 535
Db      705  AATATTTTACCTGCTGAGCTGTGAGTGTGCCACCTGCTCTCTGCAAGGCTTCCGGTCC 764
Qy      536  CATAGAGACTGCGAGGTGCTCCCTGACTCATGTGTTCCAGAGCAGAAAGTCAGAGCTC 595
Db      765  CACAGAGACTGTGAGGTGGGCCCATGCGCCACCATTTACAAAGCCAGAAAGATGAGCTC 824
Qy      596  AGTATGTGATTTCTGTATCTTGTGGAAGACAGATGAGTCCAGGCTGTGATCAGCCAG 655
Db      825  AGCGATGGCATTCGATGTGCTGTGCGAGGCAATGACCGCGTGAACAGATGATCACAG 884
Qy      656  CTGAGAGACACTGTAAACTATTTGAGAGTGTGTCAGAAAGCAGAAACAGACCTGTGT 715
Db      885  ATGAGAGAGGTGTGCGAGCTATGAGAGACATAGCCGAGAGCAGAAAGCATGTTTAAC 944
Qy      716  GAGAAATTTGATCACTATACGACATCTGAGAGAGAGAAAGCTGAATGACCCAGGCC 775
Db      945  CAGAGTTTGAAGACCTGTGCGCAGTGTGAGAGAGCGAAAGGTGAGCTGTGACGGCG 1004
Qy      776  ATCATCTGAAACAGAGAGAGAAAGTGAACATGTCCGAATCTTATCAGAAAGTATTC 835
Db      1005  CTGCGCCCGGAGCAGAAAGAGAGAGCTGACGCGGTGCGCGCTCATCTCGTCAATGTGC 1064
Qy      836  GATCACCTGAGAAAGTATCCAAAGTTGTGAGATCCAGAAATCCAGTTCAATGATGAGCC 895
Db      1065  GACCACTTGAAGGCTCTCTTAAGCTGTGAGATCTGCCATCCAGTCCATGAGAAAGCCA 1124
Qy      896  GAAATGCAATATTTCTGAGAAATGCAAGCCCTGTGCAAAAGATCTGTGAAGATCA 955
Db      1125  CAATGCGCGCTGTATCTCCAGCAGGCGCAAGAGCTATCAATTAAGGTGCGGCGCATGTG 1184
Qy      956  AAGCGTTTCAATGAGAGAAATGAAACAAGTTATGAGATCATGAGCACTTCACTGTG 1015
Db      1185  AAGGTGAGCTGCGAGGCGCGCGAGCCAGGCTATGAGAGCATGAGAGCAATTCACCGTA 1244
Qy      1016  AATCTCAATGAGAAAGAAATTTATCCGTGAATGACTTTTCTAGAGAAAGAGAG 1075

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Db 1245 AGGTGGAGCAGTGGCCGAATGCTGGGACCATCGACTTCAGCCAGCGCTTCCGGG 1304
Qy 1076 GAAGAGATGAGAGGAATATAGATAGAGAGAGAGAGATGACAGTAAAG 1130
Db 1305 GAGAGAGAGAGGTGGCCCGCCAGACGAGAGAGAGGCGACGCGGGCCGAGAGAG 1359

RESULT 11
US-10-061-043A-20
; Sequence 20, Application US/10061043A
; Publication No. US20030129686A1
; GENERAL INFORMATION:
; APPLICANT: Glaxo, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753B
; CURRENT APPLICATION NUMBER: US/10/061,043A
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 1053
; TYPE: DNA
; ORGANISM: rat
US-10-061-043A-20

Query Match 17.5%; Score 452; DB 15; Length 1053;
Best Local Similarity 66.1%; Pred. No. 6.4e-111;
Matches 669; Conservative 0; Mismatches 340; Indels 3; Gaps 1;
Qy 126 CCATGATTAATCTGGAAAGCAATGATCTGTCCATCTGCTAGAGATGTTCAAGAGC 185
Db 38 CTATGAGAACCTGGAGAGAGAGCTCATCTGCCCATCTGAGATGTTACCAAGC 97
Qy 186 CTGGTGATCTTCCCTTGGCAGCAGCACTGTGAGAGAAATGTCGACATCTTCC 245
Db 98 CTGGTGATCTTCCCTTGGCAGCAGCACTGTGAGAGAAATGTCGACATCTTCC 157
Qy 246 AGGCTCTAACCCGTAATCTTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 305
Db 158 AGGCTCTAACCCGTAATCTTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 217
Qy 306 TCCGCTGTCCCTCTGCAAGACATGAGTGTGTGAAGAGAGAGAGAGAGAGAGAG 365
Db 218 TCCGCTGTCCCTCTGCAAGACATGAGTGTGTGAAGAGAGAGAGAGAGAGAGAG 277
Qy 366 AGAGGAACCTGCTCTGAGAGAAACATTAATGATTAAGAGAGAGAGAGAGAGAGAG 422
Db 278 AGAGGAACCTGCTGAGAGAAACATTAATGATTAAGAGAGAGAGAGAGAGAGAGAG 337
Qy 423 CAGAAAAAATTTGAGACAGCCATGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 482
Db 338 CCCTGAG 397
Qy 483 ATTGTCTGAATCTGTAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 542
Db 398 ACTGTCTACGTCGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 457
Qy 543 ACTGCAAGTGTGCTCCCTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 602
Db 458 CTTGAGAGTGTGCTCCCTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 517
Qy 603 GTATGCTGTAATCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 662
Db 518 GCATCTCATGCTGTGAG 577

Qy 663 ACACCTGTAATACTATTGAGAGAGTCTGACAGAAACAGAGAGAGAGAGAGAGAGAG 722
Db 578 ACTCTGTCGAGATGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 637
Qy 723 TTGATCACTTAATGAGAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 782
Db 638 TTGAGCCCTCTTACGCAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 697
Qy 783 GAACAG 842
Db 698 AG 757
Qy 843 TGGAGAAAGTATCCAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 902
Db 758 TGGAGAAAGTATCCAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 817
Qy 903 CAGATTTCTGAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 962
Db 818 CCACCTTCTCTTGAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 877
Qy 963 TTGATGAG 1022
Db 878 GCGAGCTGGGAG 937
Qy 1023 ATGAG 1082
Db 938 AACACATAG 997
Qy 1083 ATGAG 1134
Db 998 CTGAG 1049

RESULT 12
US-10-060-634C-20
; Sequence 20, Application US/10060634C
; Publication No. US20030219739A1
; GENERAL INFORMATION:
; APPLICANT: Glaxo, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753A
; CURRENT APPLICATION NUMBER: US/10/060,634C
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 1053
; TYPE: DNA
; ORGANISM: rat
US-10-060-634C-20

Query Match 17.5%; Score 452; DB 17; Length 1053;
Best Local Similarity 66.1%; Pred. No. 6.4e-111;
Matches 669; Conservative 0; Mismatches 340; Indels 3; Gaps 1;
Qy 126 CCATGATTAATCTGGAAAGCAATGATCTGTCCATCTGCTAGAGATGTTCAAGAGC 185
Db 38 CTATGAGAACCTGGAGAGAGAGCTCATCTGCCCATCTGAGATGTTACCAAGC 97
Qy 186 CTGGTGATCTTCCCTTGGCAGCAGCACTGTGAGAGAAATGTCGACATCTTCC 245
Db 98 CTGGTGATCTTCCCTTGGCAGCAGCACTGTGAGAGAAATGTCGACATCTTCC 157
Qy 246 AGGCTCTAACCCGTAATCTTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 305
Db 158 AGGCTCTAACCCGTAATCTTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 217